

09973025-101001

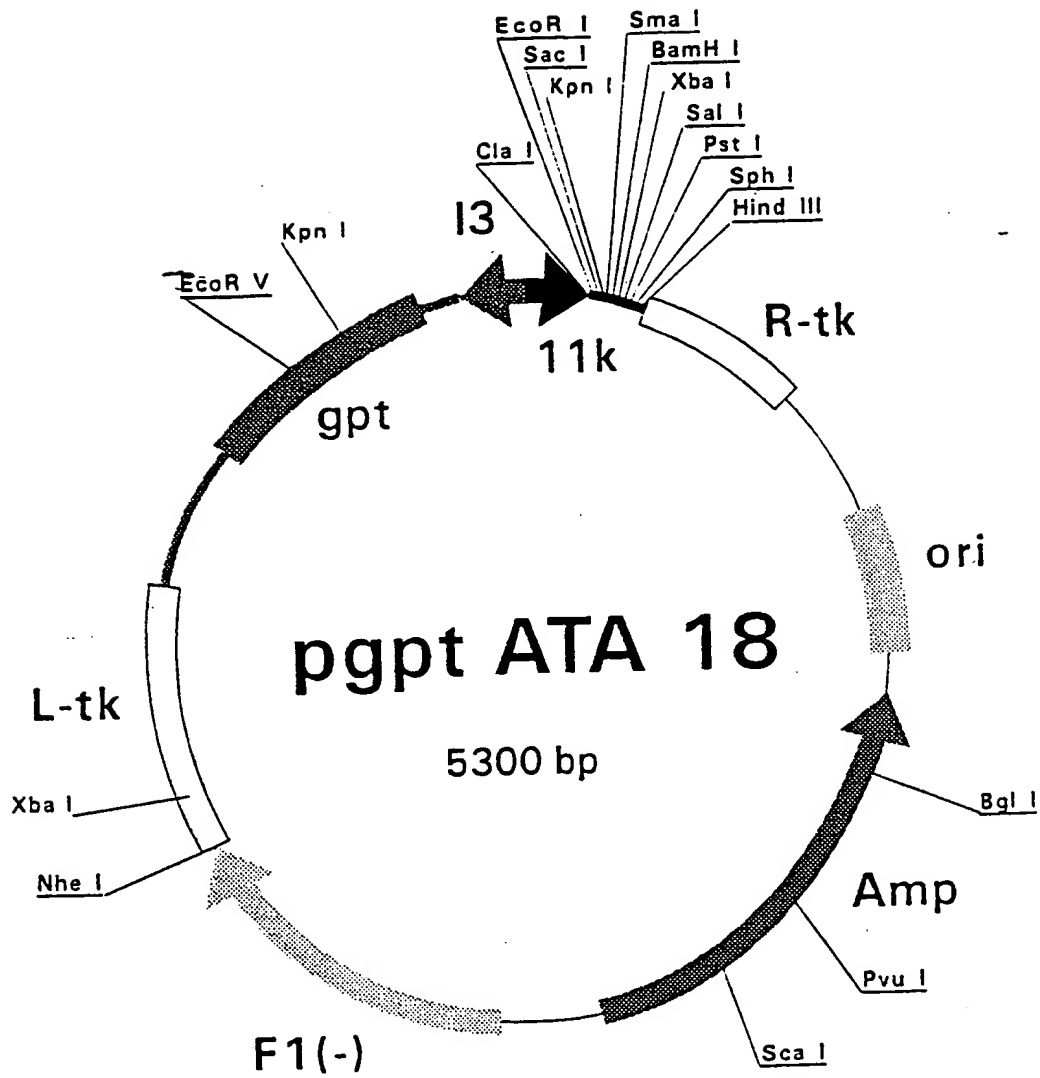


Fig. 1

09973025-101001

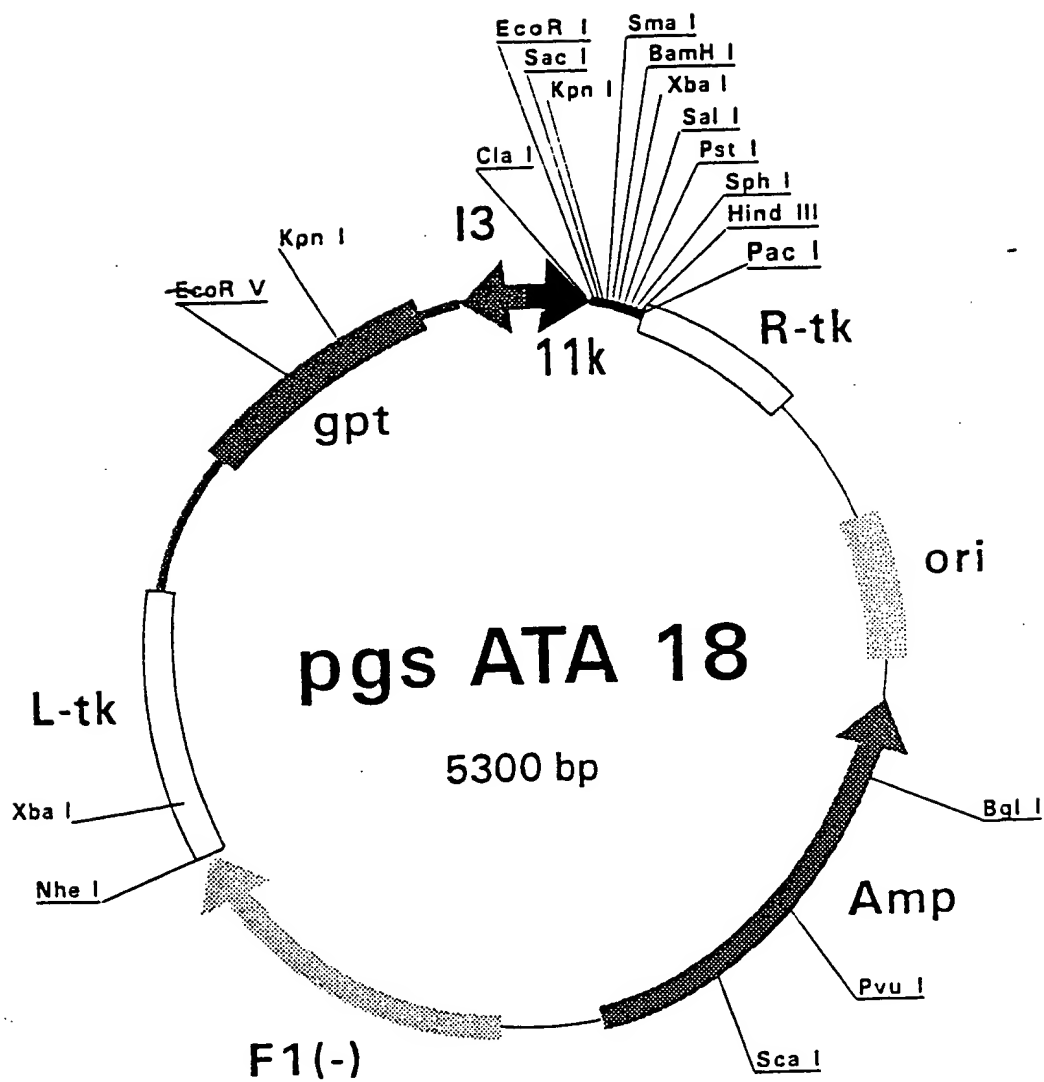


Fig. 2

09973025.101001

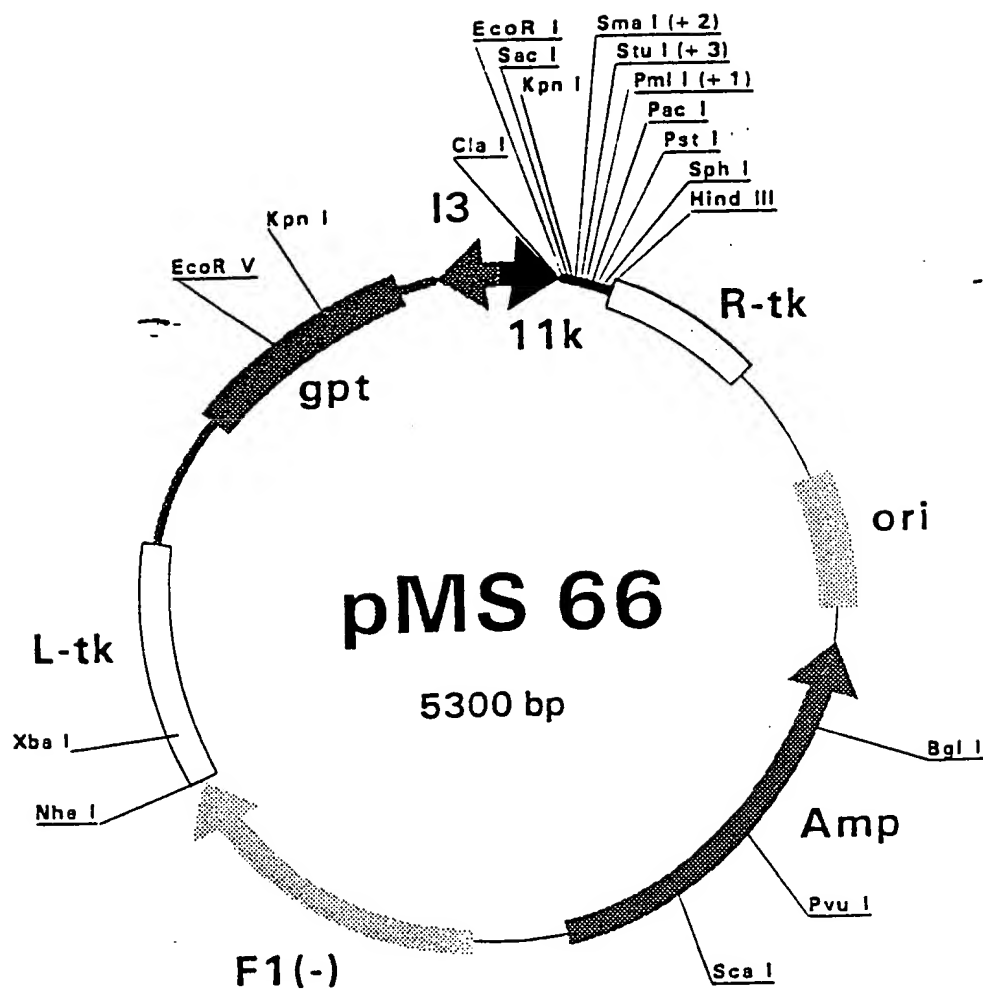


Fig. 3

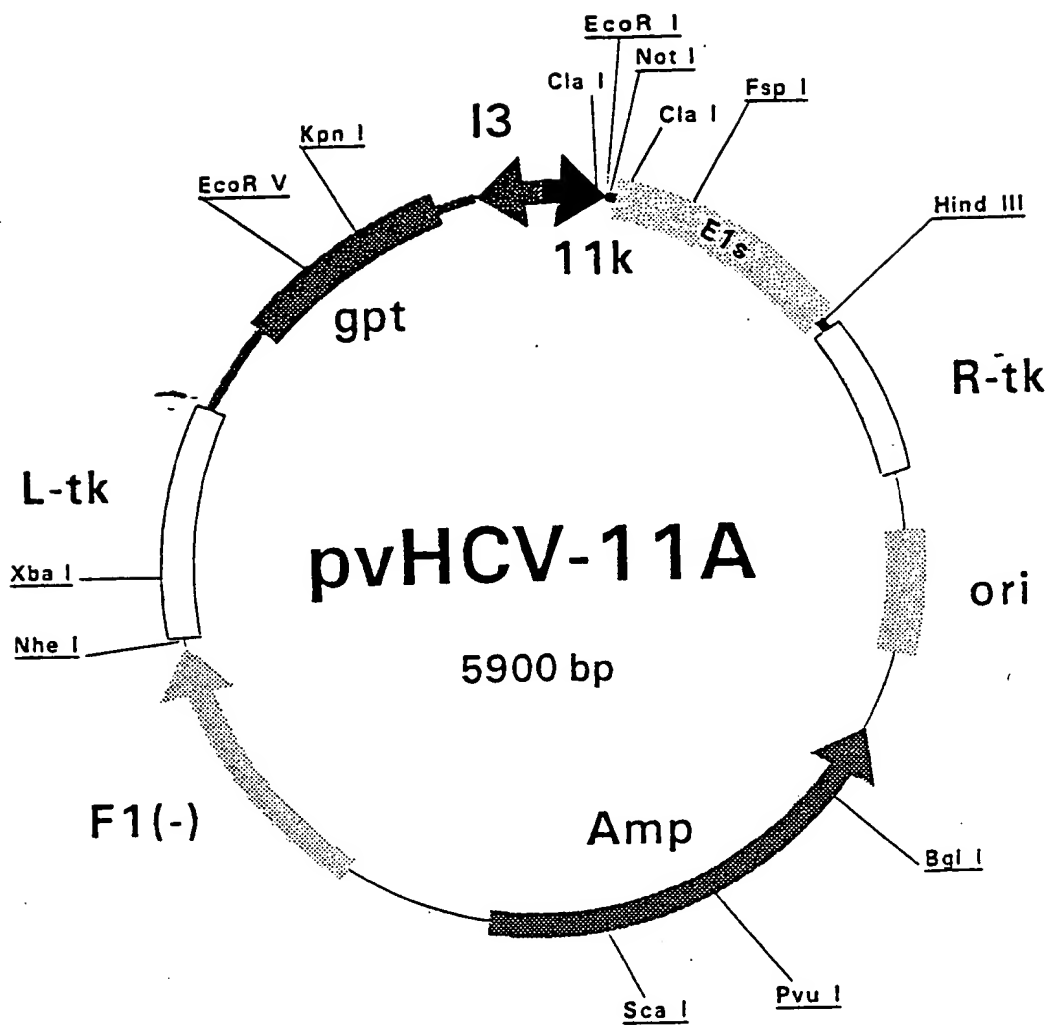


Fig. 4

Anti-E1 levels in NON-responders to IFN treatment

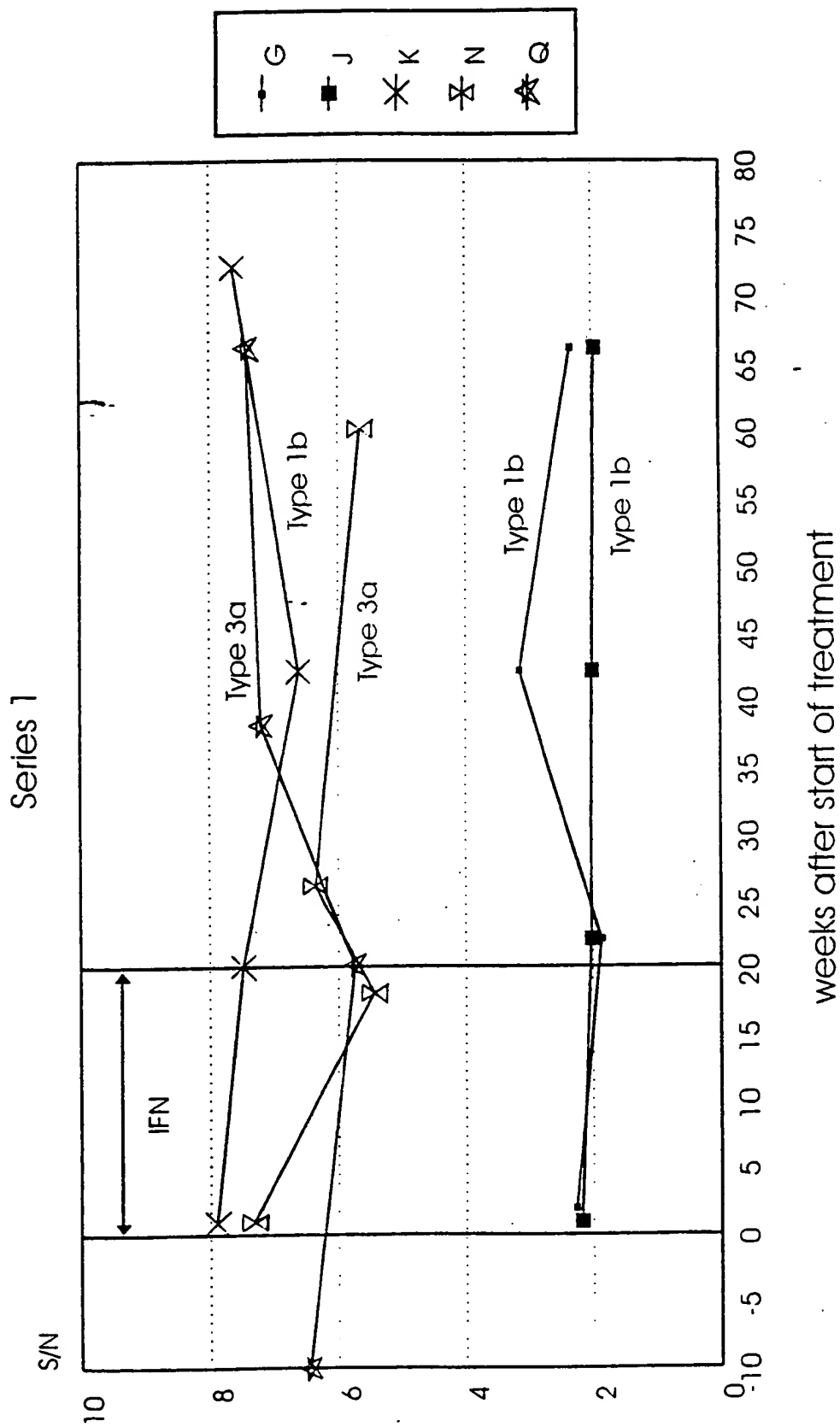
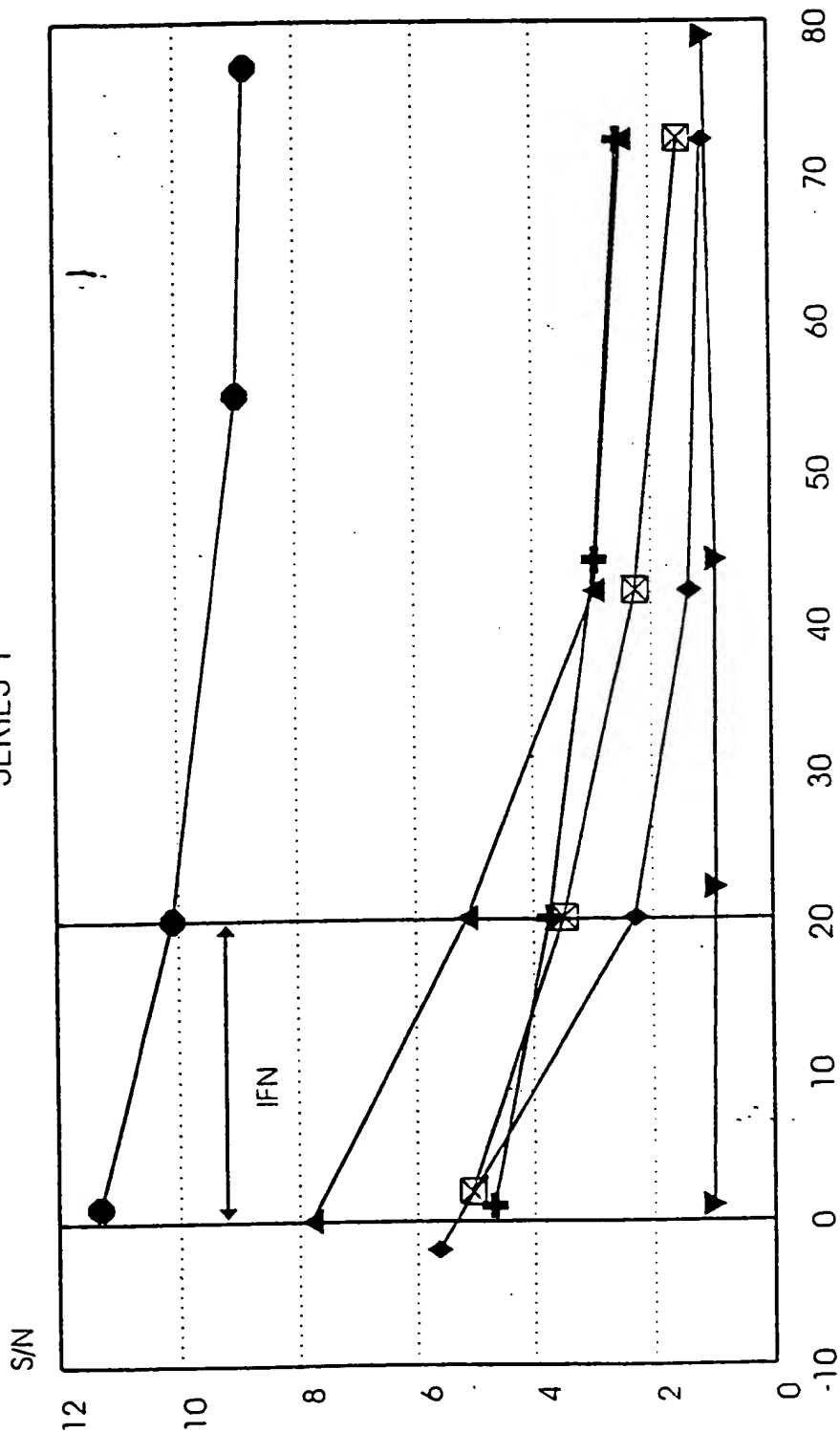


Fig. 5

Anti-E1 levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig. 6

Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2

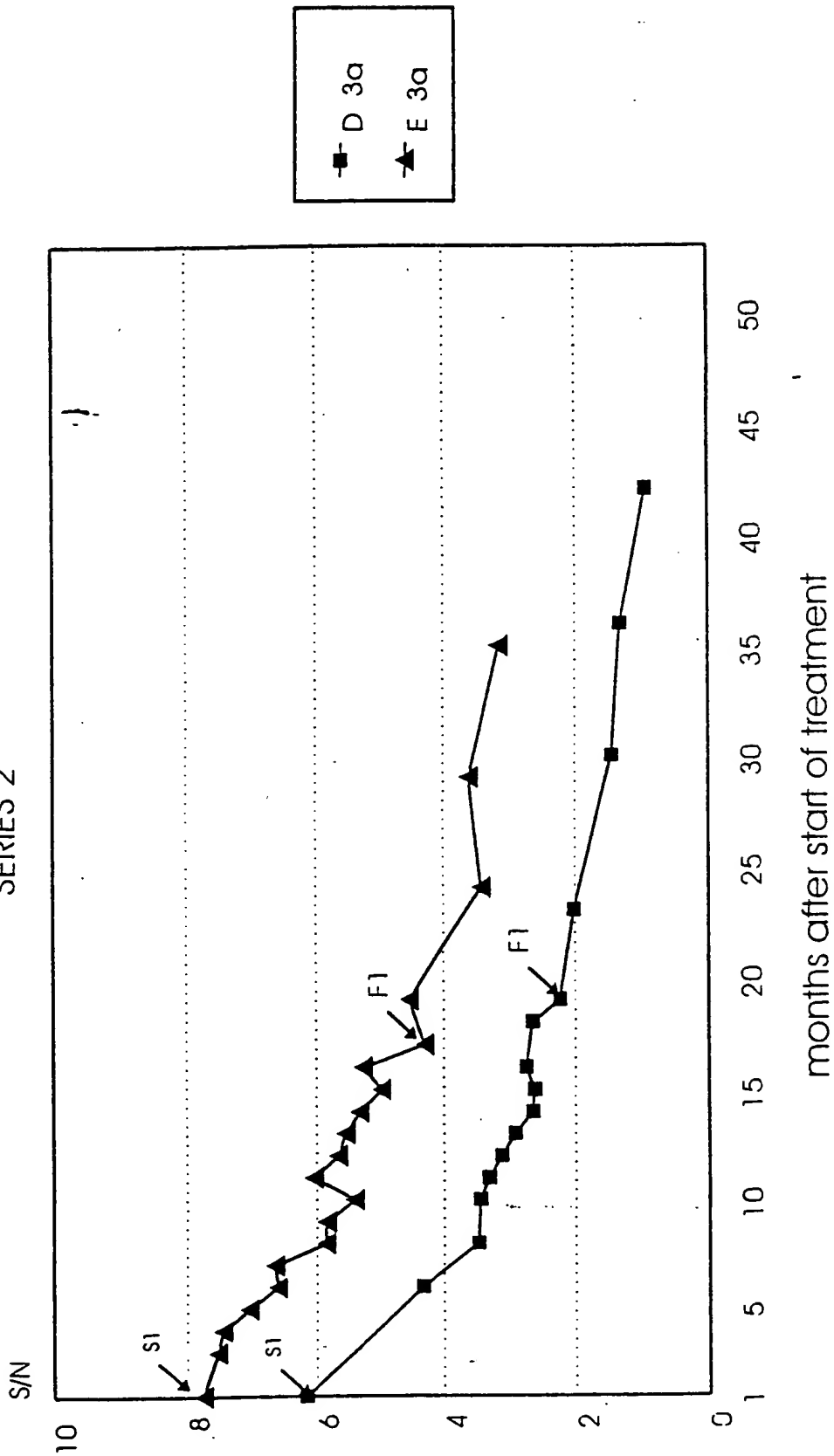
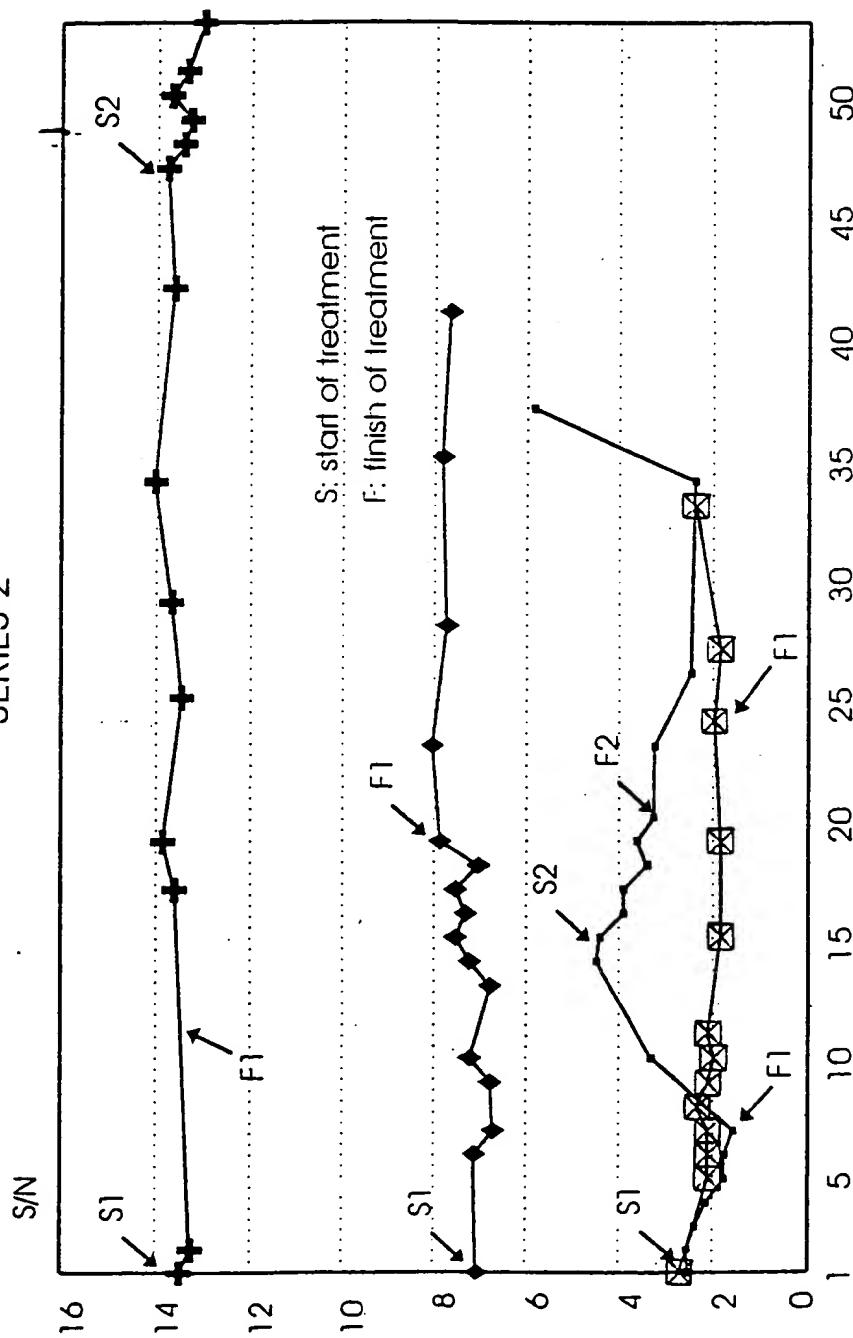


Fig. 7

Anti-E1 levels in INCOMPLETE responders to IFN treatment

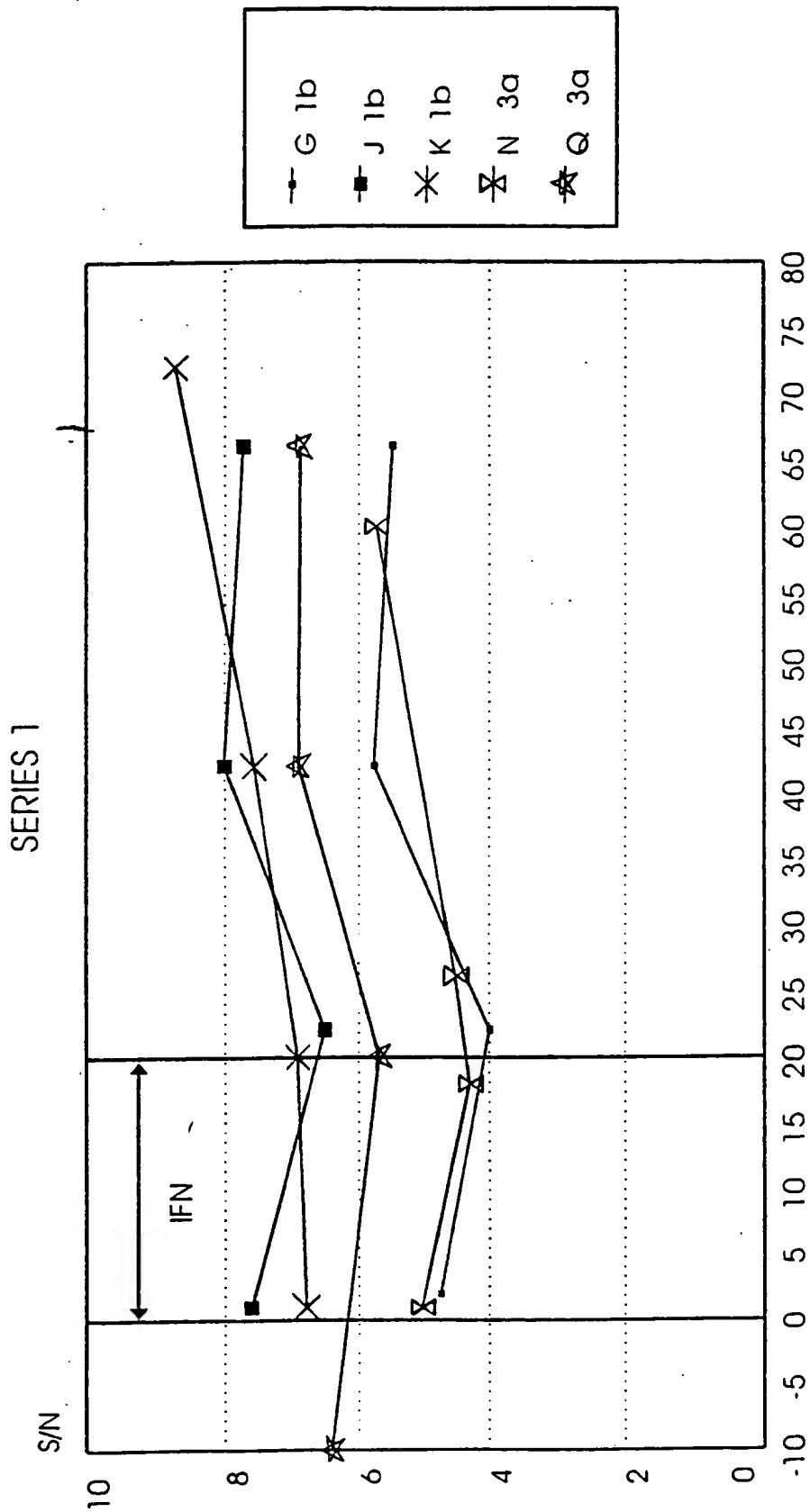
SERIES 2



months after start of treatment

Fig. 8

Anti-E2 levels in NON-RESPONDERS to IFN treatment

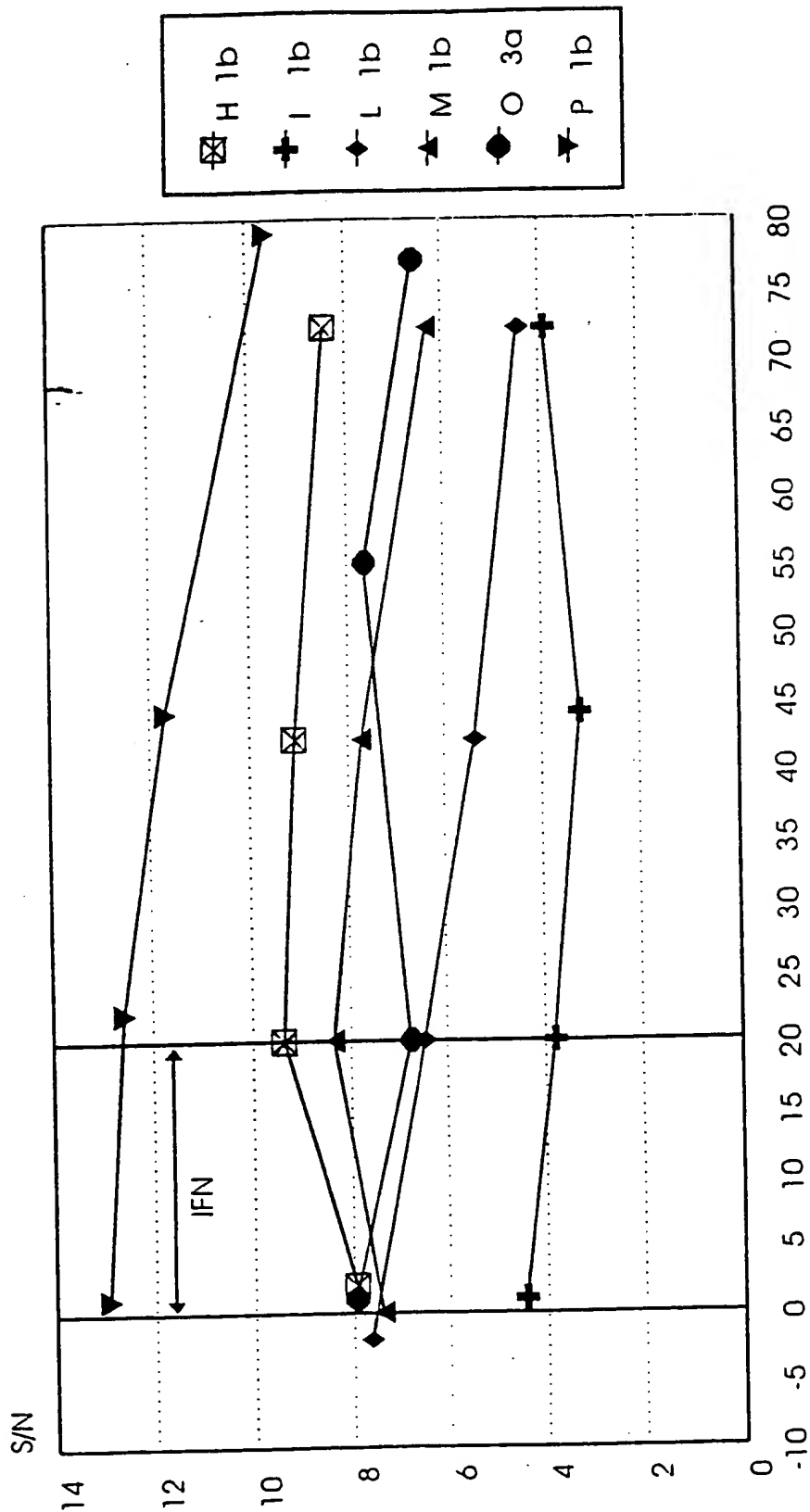


weeks after start of treatment

Fig. 9

Anti-E2 levels in RESPONDERS to IFN treatment

SERIES 1

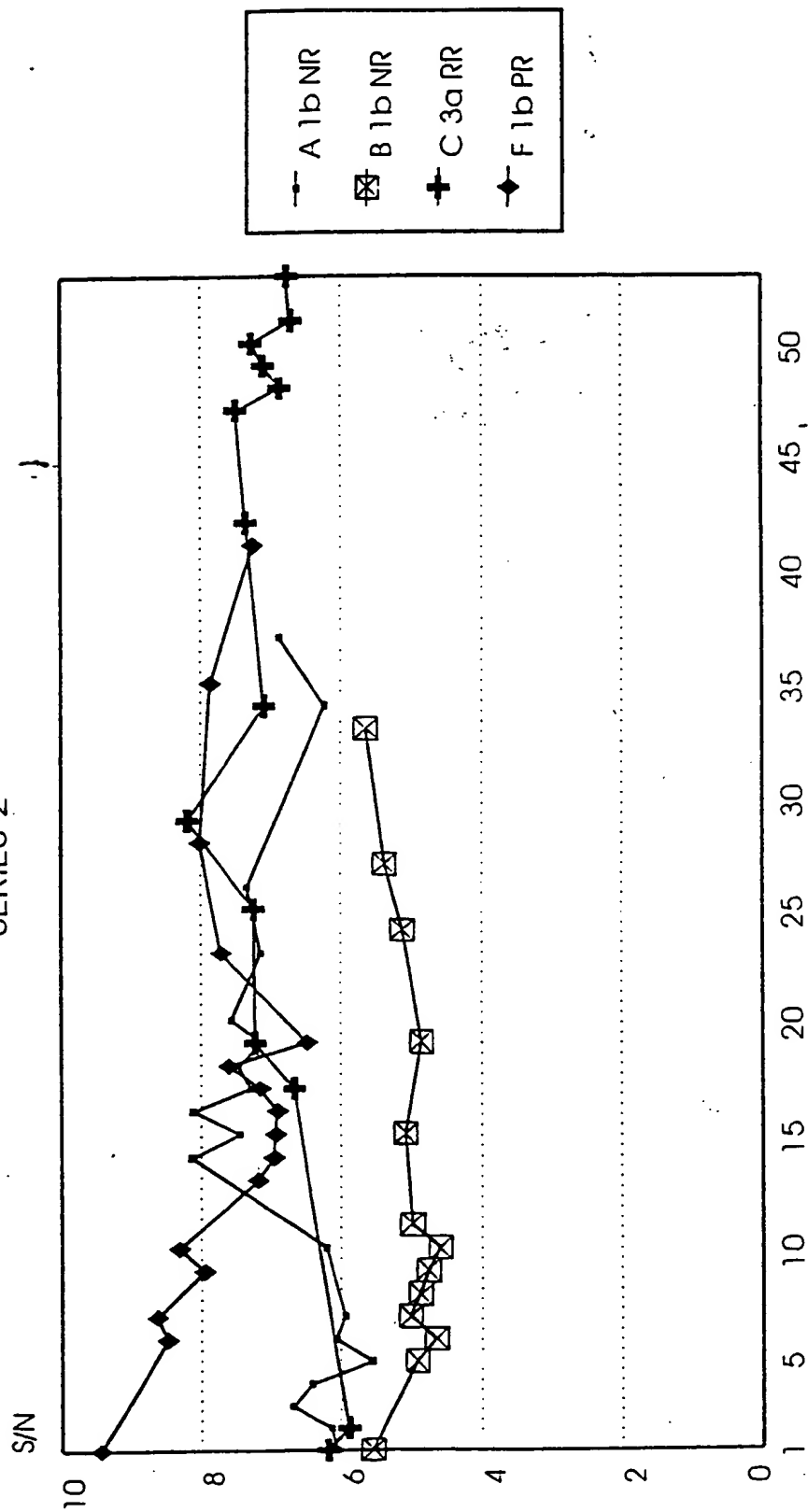


weeks after start of treatment

Fig.10

Anti-E2 levels in INCOMPLETE responders to IFN treatment

SERIES 2

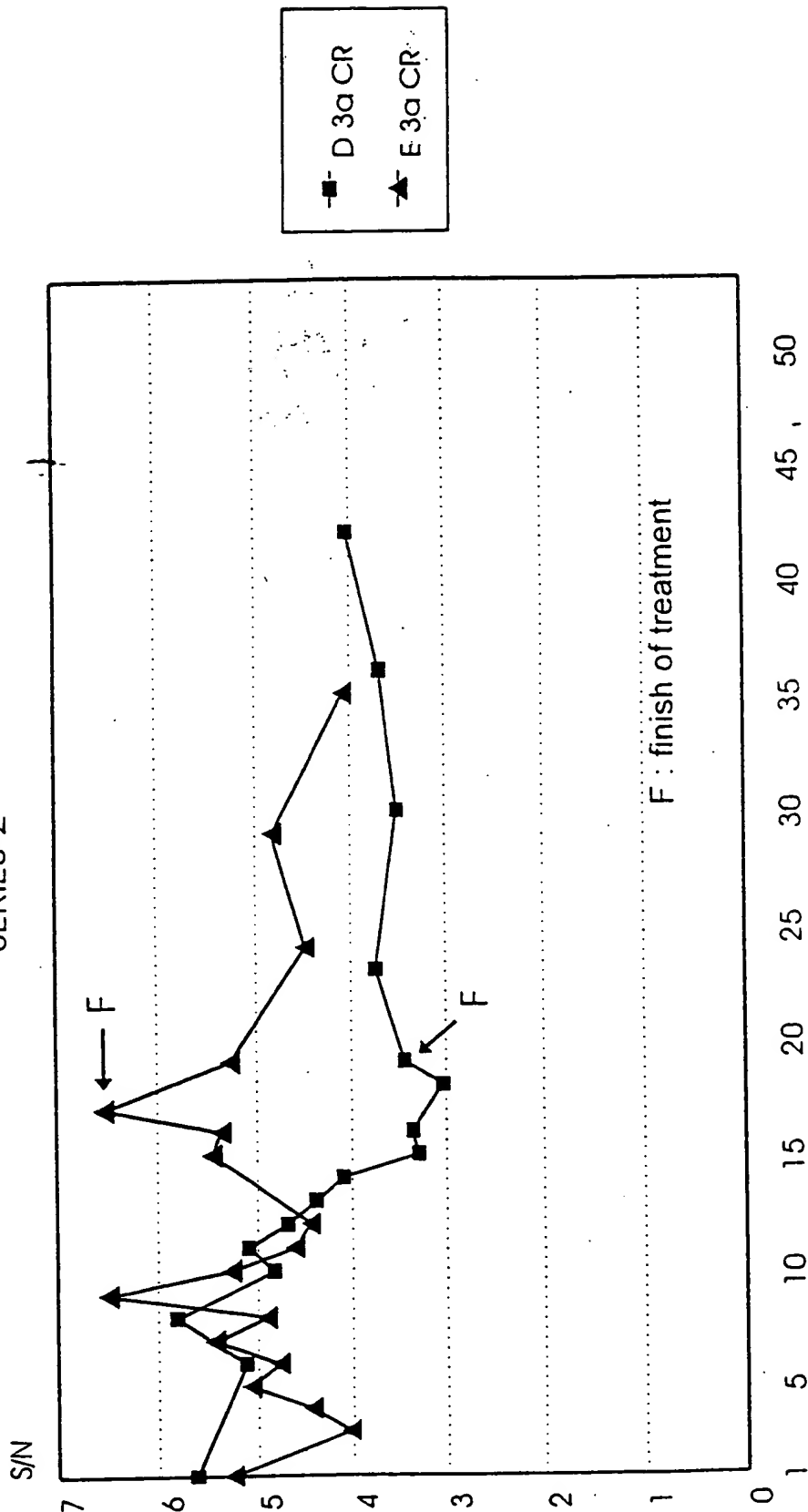


months after start of treatment

Fig.11

Anti-E2 levels in COMPLETE responders to IFN treatment

SERIES 2



months after start of treatment

Fig.12

Human anti-E1 reactivity competed with peptides

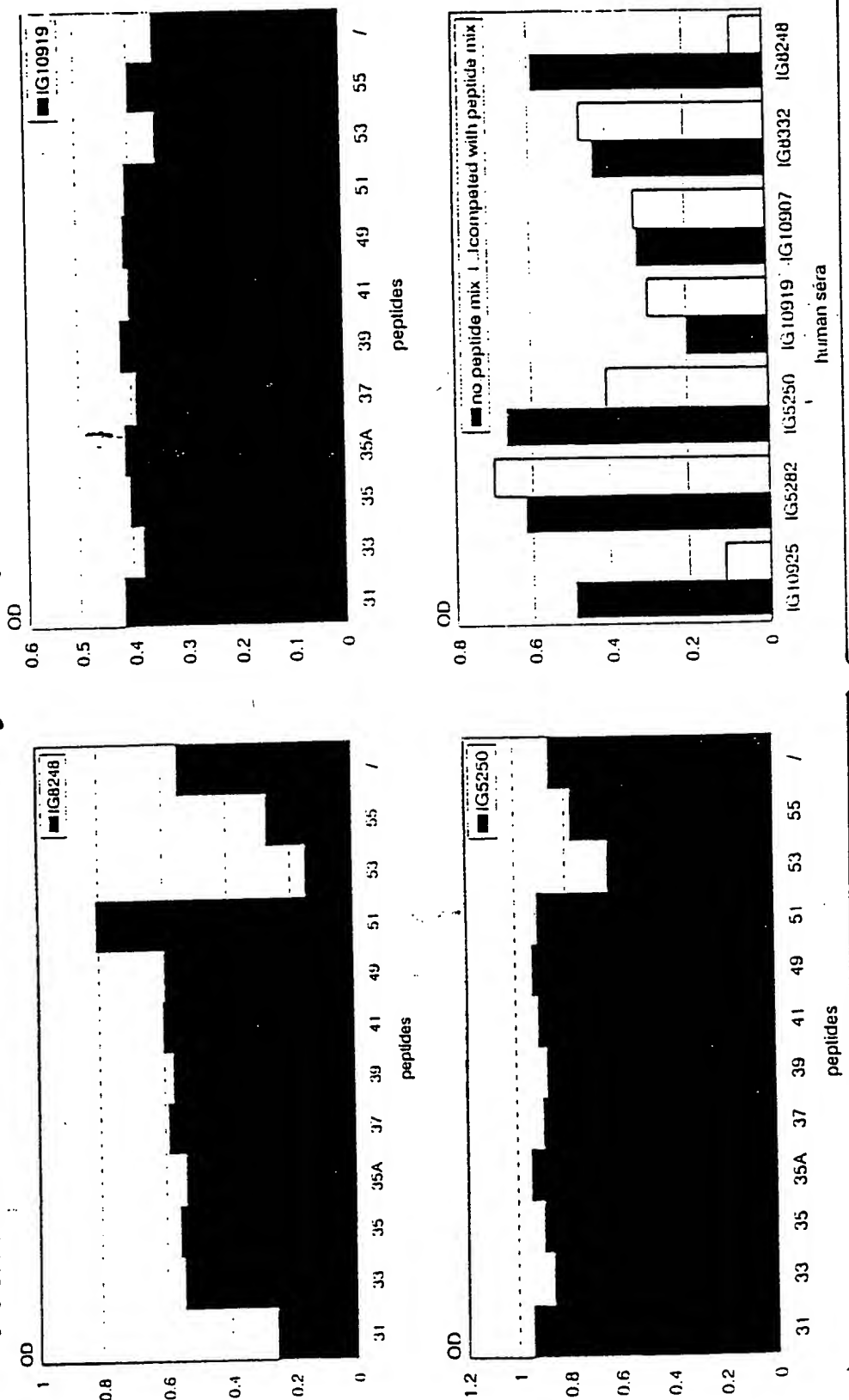


Fig.13

Competition of reactivity of anti-E1 Mabs with peptides

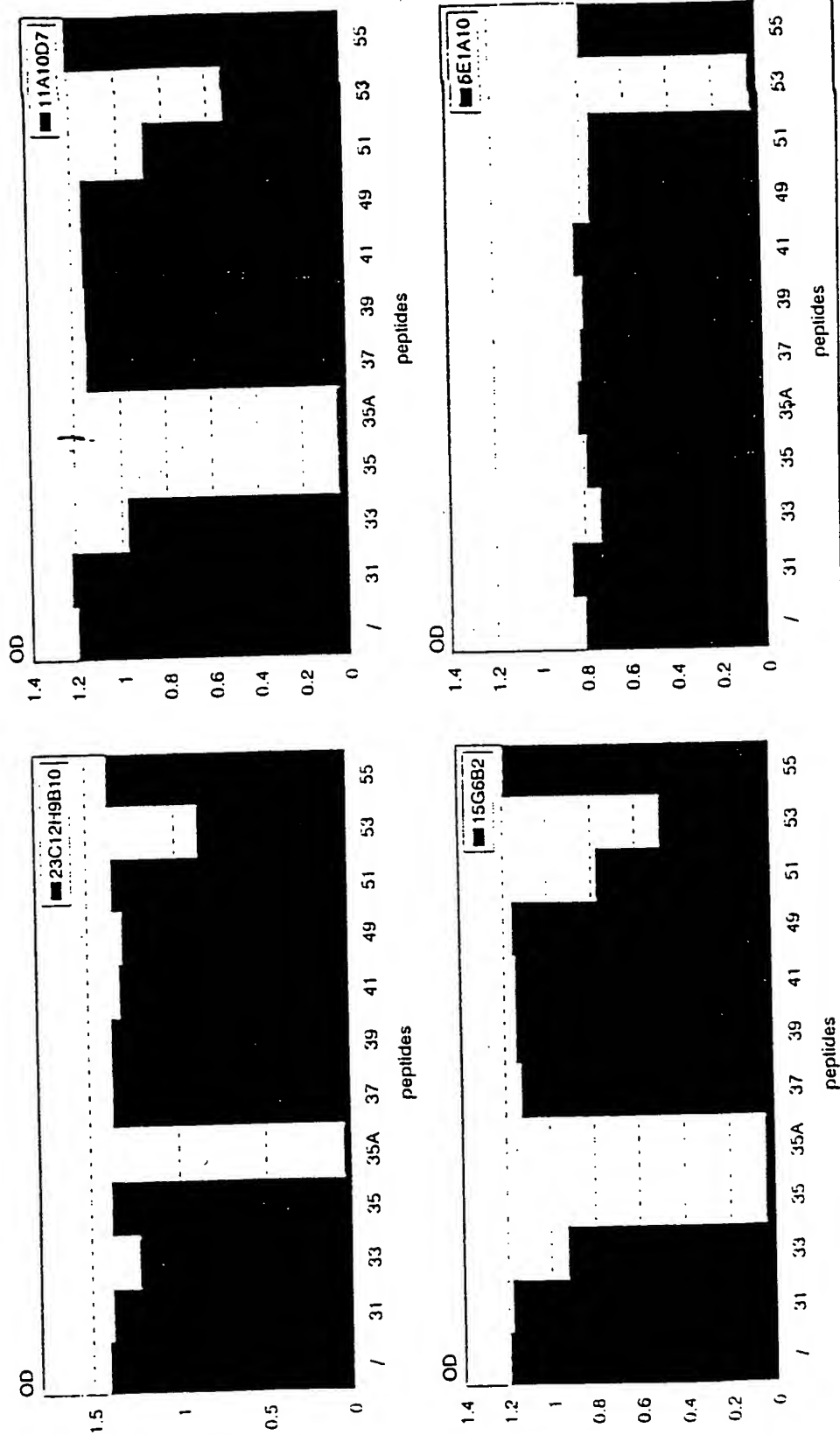
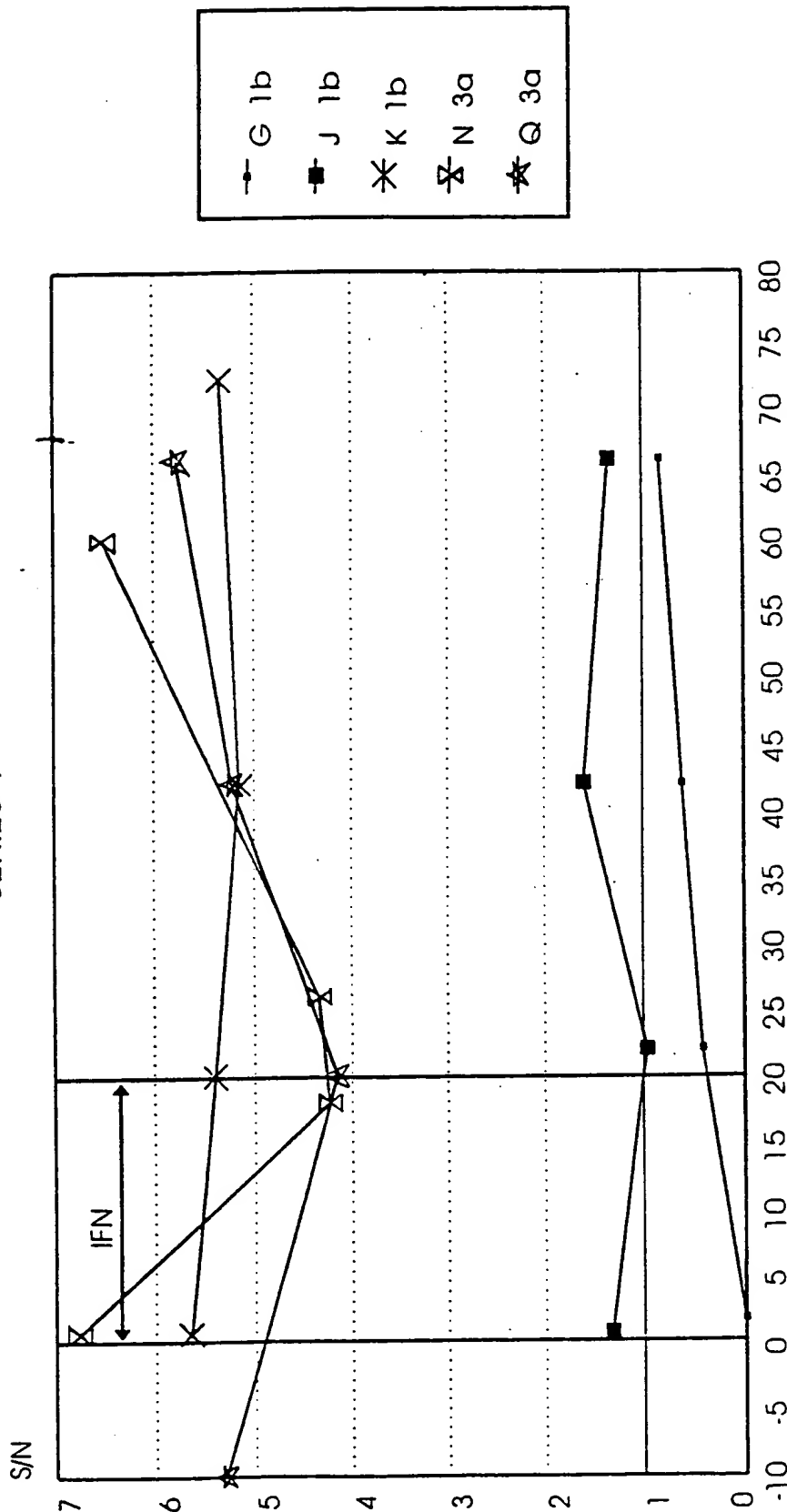


Fig.14

Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.15

Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

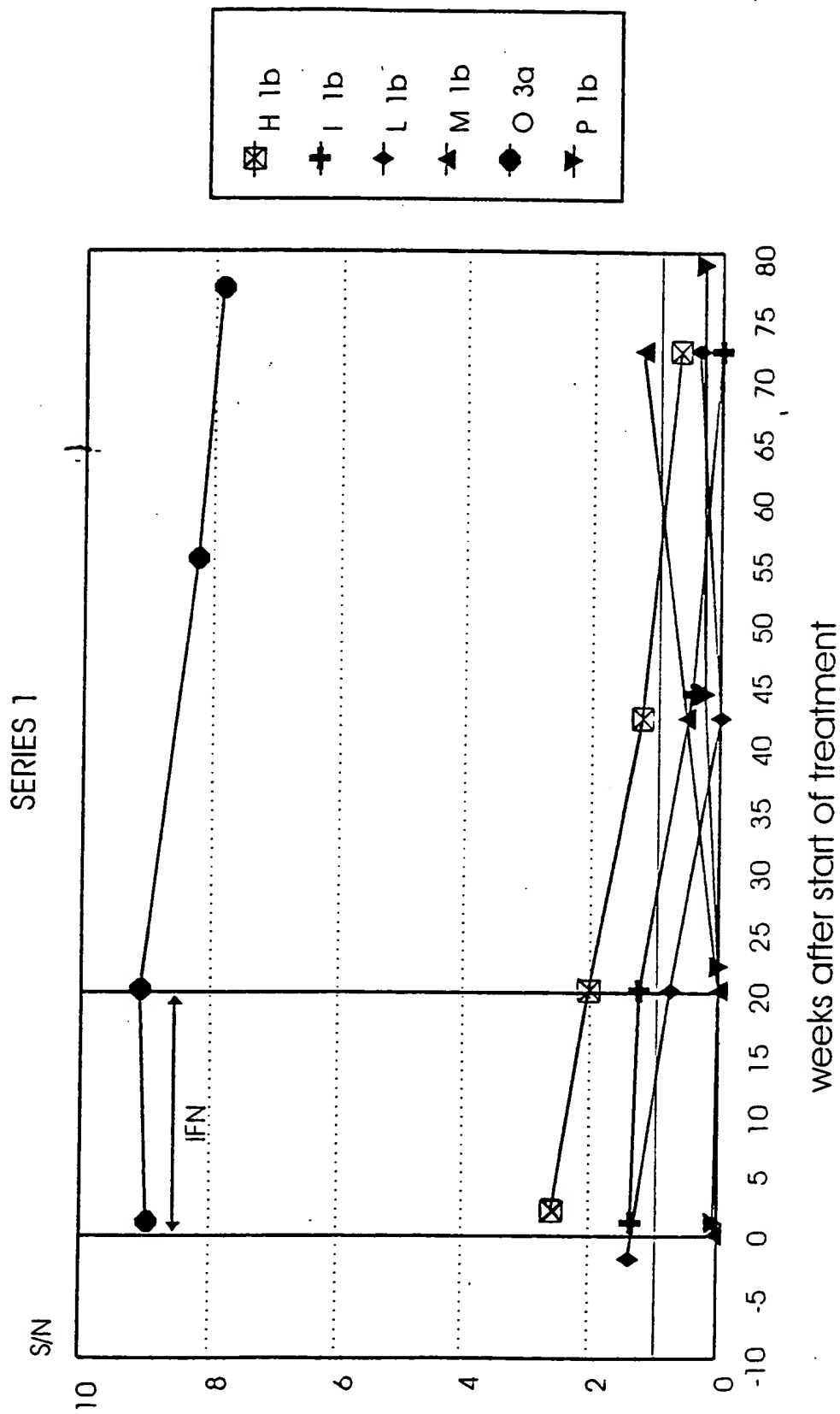


Fig.16

Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

SERIES 1

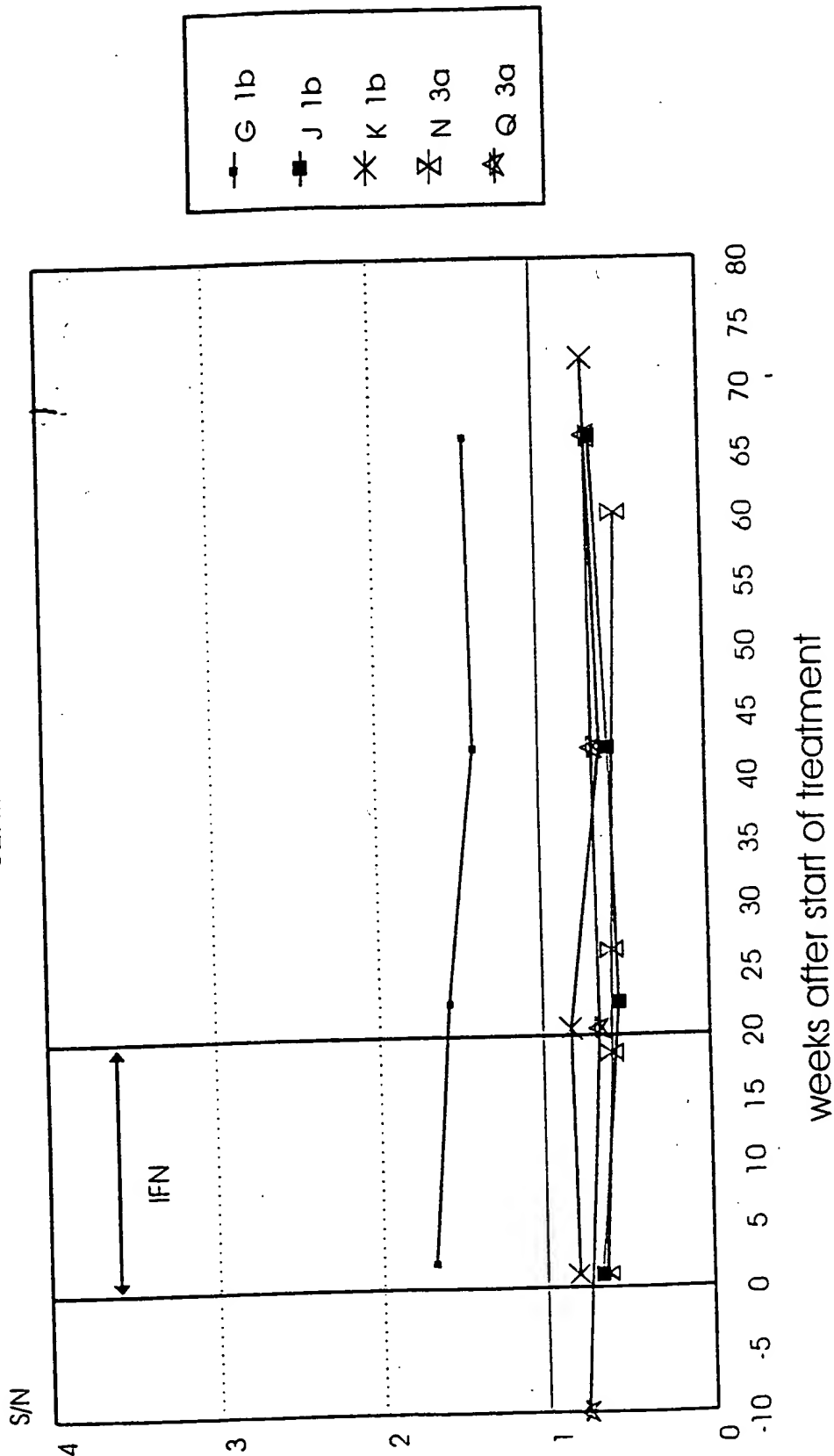
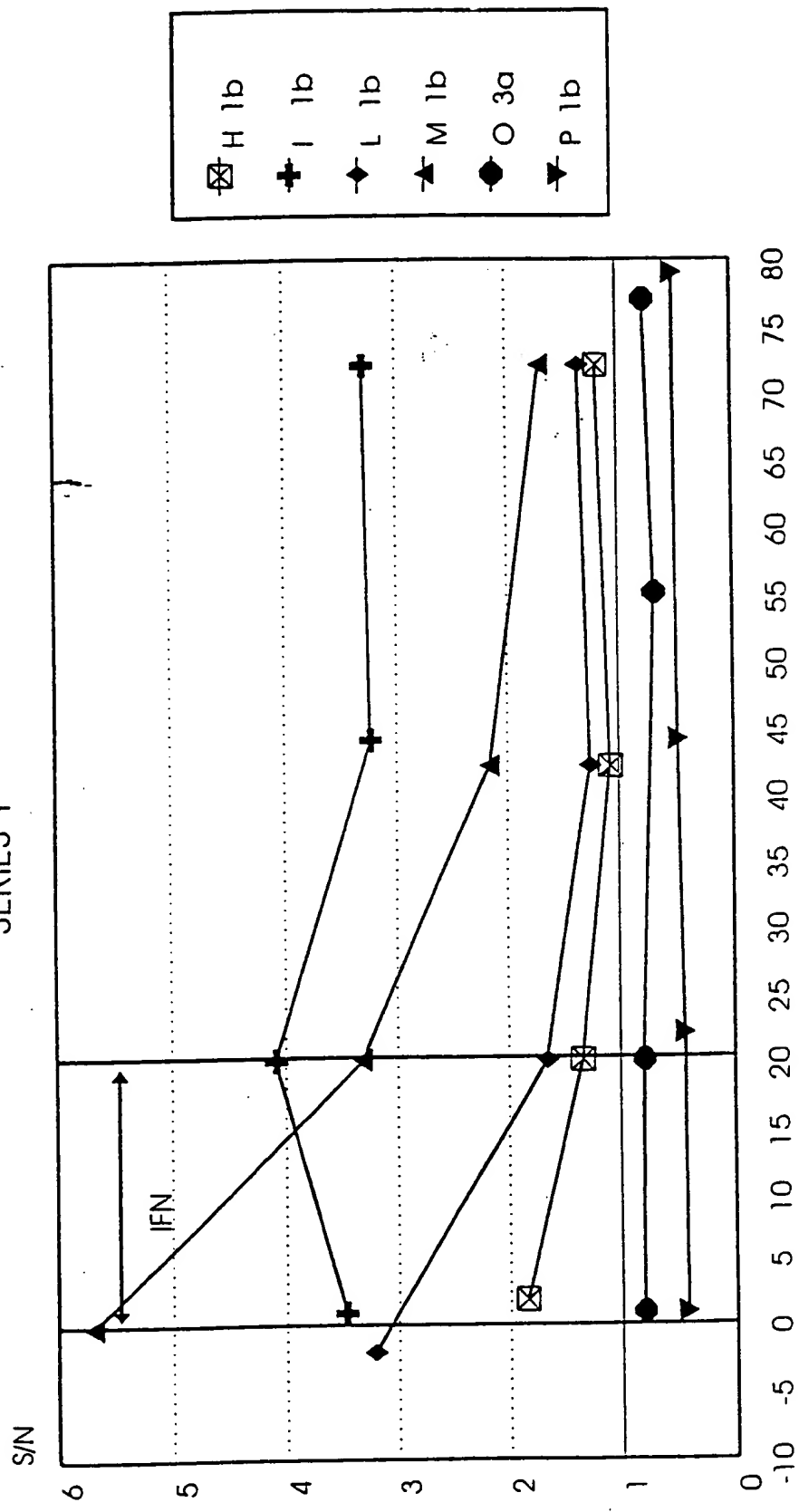


Fig.17

Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.18

Competition of reactivity of anti-E2 Mabs with peptides

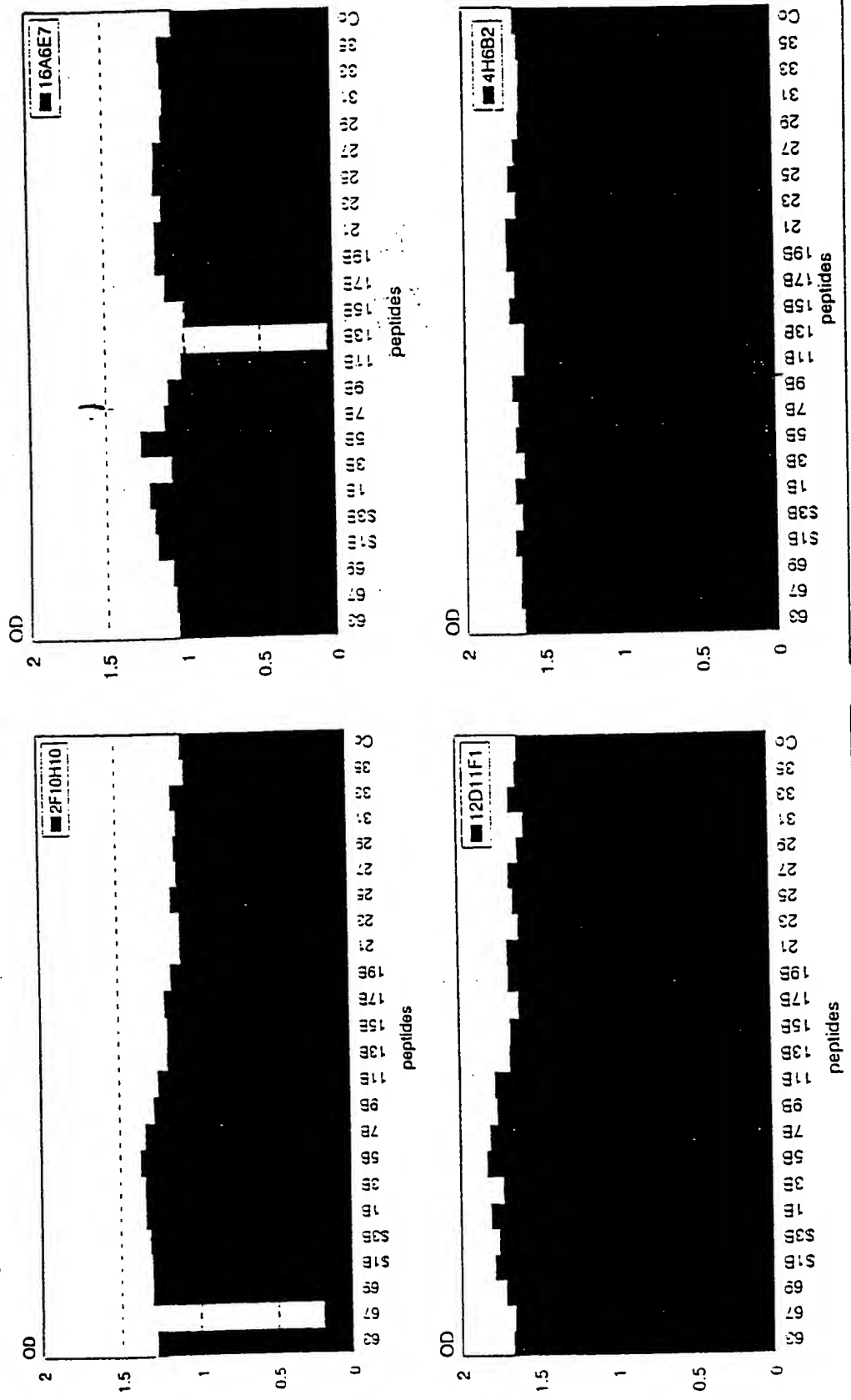


Fig.19

Human anti-E2 reactivity competed with peptides

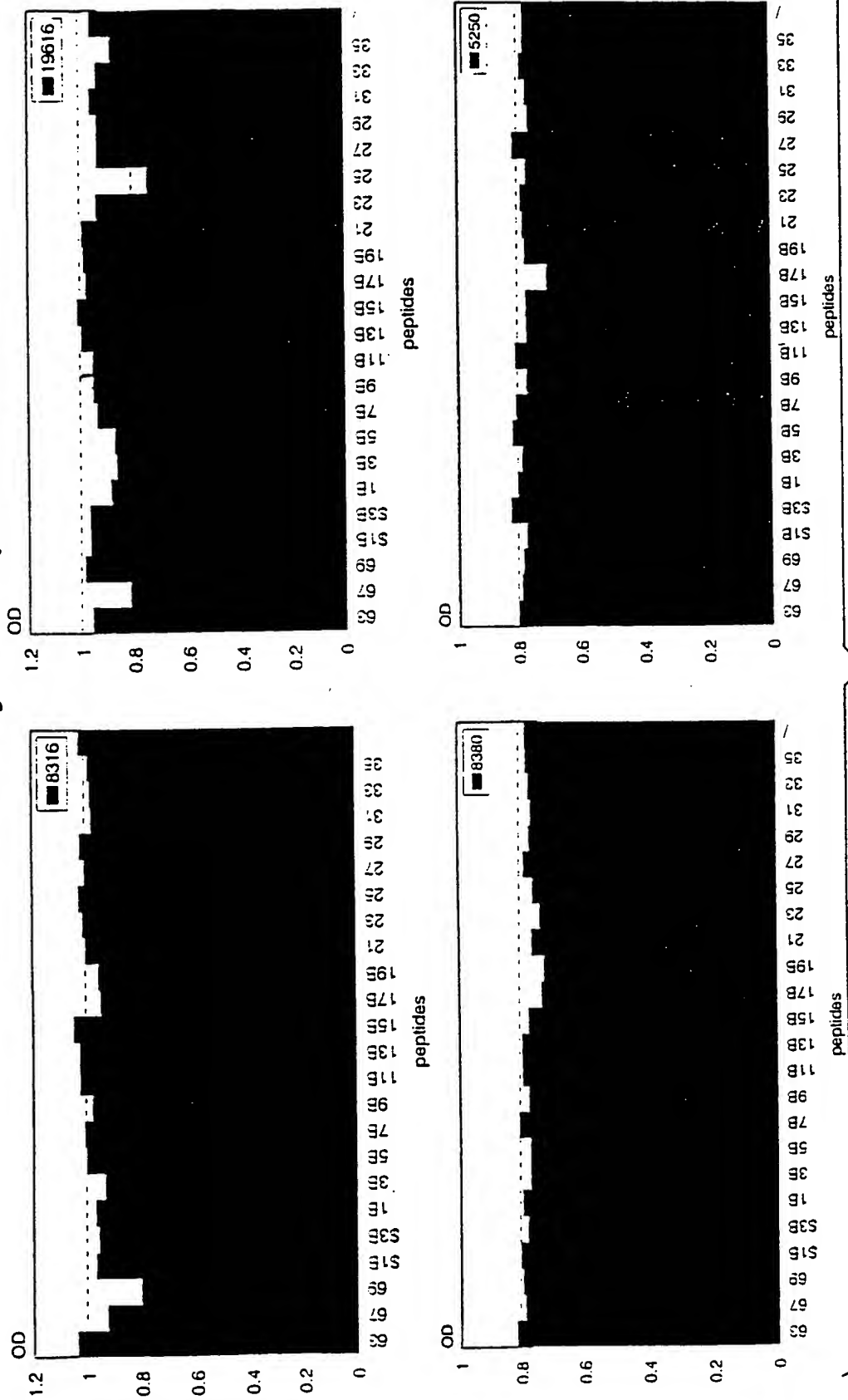


Fig. 20

Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)

3'ACGTCCGTACGTTCTGAATTAATTAATCGA5' (SEQ ID NO 94)

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCACCATCACTAATAGT
TAATTAACTGCA 3' (SEQ ID NO 2)

3'CCTCCGGACGTGCACTAGCTCCCGTCTGTGGTAGTGGTGGTAGTGATTATCAATTAATTG
5' (SEQ ID NO 95)

SEQ ID NO 3 (HCC19A)

ATGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTACTGTCCTGTCTGACCATTCCA
GCTTCCGCTTATGAGGTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCT
CCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCCGGGAGAACAACCTCTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTC
GCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTGATTTGCTCG
TTGGGGCGGCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTC
CTCGTCTCCCAGCTGTTCAACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCA
ATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGAT
GAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCT
GTCGTGGACATGGTGGCGGGGGCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATT
CCATGGTGGGGAACGGGCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG

SEQ ID NO 5 (HCC110A)

ATGTTGGGTAAGGTCATCGATACCCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTG

Fig. 21B

TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCTGGACATGGTGGCGG
GGGCCATTGGGGAGTCCTGGCGGGTCTCGCCTACTATTCCATGGTGGGGAAGTGGGC
TAAGTTTTGATTGTGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 7 (HCC11A)

ATGTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCG
GGTCTGGAAGACGGCGTGAAGTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGC
AACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAACA
ACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGT
CCCCACTACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCAAC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 9 (HCC12A)

ATGCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCT
CCAACTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTGATTTGCTC
GTTGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTGTTTTCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTCCTAATAG

SEQ ID NO 11 (HCC13A)

ATGTCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCT
CCAACTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT

09973025-101001

Fig. 21C

GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTTGTTTCCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

ATGCTGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAAGTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGC
AACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACA
ACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAACGCCAGCAT
CCCCACTACAACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTACC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCP_r51)

ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCP_r52)

ATGTTGGGTAAAGGTCATCGATACCCT

SEQ ID NO 17 (HCP_r53)

CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCP_r54)

CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCP_r107)

ATACGACGCCACGTGATTCAGCTGTTACCATC

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Fig. 21D

SEQ ID NO 20 (HCP108)

GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCC137)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCGGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGCGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCATTGGGG
AGTCCTGGCGGGTCTCGCCTACTATTCCATGGTGGGGAACGGCTAAGGTTTTGATTG
TGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 23 (HCC138)

ATGTTGGGTAAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGCGATTCCCAGCTGTTACCATCTCGCCTCG
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CACCGTATGGCTTGGGATATGATGATGAACTGGTAA
TAG

SEQ ID NO 25 (HCC139)

ATGTTGGGTAAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT

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Fig. 21E

ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGCGATTCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTCTAATAG

SEQ ID NO 27 (HCCI40)

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTCTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGCGATTCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCGTGATCGAGGGCAGACACCATCACCAACCATCACTAATAG

SEQ ID NO 29 (HCCI62)

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CGCTCGTCGGCGCTCCCGTAGGAGGCGTCGAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAATTTGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCCGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAAGTGTGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGATATGATGATGAACTGGTAATAG

Fig. 21F

SEQ ID NO 31 (HCCI63)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTGCGCGATCTCATGGGGTATATCC
CGCTCGTAGGCGGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACCTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCP109)

TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCP72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

TGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC
GGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGG
GCCTCGCCTACTATTCCATGGTGGGGAACCTGGGCTAAGGTTTTGGTTGTGATGCTACTC
TTTGCCGGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCA
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CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG
CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT

Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCTTCACCACCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCTCATCAAATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCC
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CACCACGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCCI41)

GATCCACAAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT
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GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG
CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTGCTCAGGGGTGGGGTCCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATTAATTAG

SEQ ID NO 39 (HCCI42)

GATCCACAAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT

Fig. 21H

TTGCCGGCGTCGACGGGCATACCCGCGTGTGTCAGGAGGGGCAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCTGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG
CGCTTGGCCAGCTGTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
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CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
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TCGGGGGGGCGGCAACAACACCTTGACCTGCCCCACTGAETGTTTTCGGAAGCACCC
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TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTTGAAGCCGCATGCAATTGGACTCG
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TCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 41 (HCCI43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT
CTTTAGCCCCGGGTCTGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTG
CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC
GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAACACGCGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGG
GGGCGTGGAGCACAGGTTTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG
CAGAGCTTAATTAATTAG

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Fig. 21I

SEQ ID NO 43 (HCCI44)

ATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT
CTTAGCCCCGGGTGCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCG
CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCCTCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC
GACCGATCGGTTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAACACGCGGCCGCGGAGGCAACTGGTTCGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG
GGGCGTGGAGCACAGGTTTCGAAGCCGCATGCAATTGGAAGTTCGAGGAGAGCGTTGTGA
CTTGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGGTGAT
CGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 45 (HCCL64)

ATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGG
GGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATAC
CCGCGTGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGC
CCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAAC
AGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCT
ACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCTCCAT
CGACAAGTTCGCTCAGGGGTGGGGTCCCCCTCACTTACACTGAGCCTAACAGCTCGGAC
CAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTC
AGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGA
TCGGTTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTC
AACAAACACGCGGCCGCGGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACT
GGGTTACCAAGACGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAAC
ACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGAT
GCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGG
CACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCG

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Fig. 21J

TGGAGCACAGGTTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGA
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATA
CTGCCCTGTTCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTC
ATCAAATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGC
CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTG
GTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTTGTGTTCTT
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCCTTCTAT
GGCGTGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

SEQ ID NO 47 (HCC165)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTG
TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG
GGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACCTGGGC
TAAGGTTTTGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTGAG
GAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGC
TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT
GAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA
TTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCCG
CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA
CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT
CCAGTGTATTGCTTACCCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGTGT
CCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG
CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTACCAAGA
CGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCGGCAACAACACCTTGACCTGCC

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Fig. 21K

CCACTGACTGTTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCC
CTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGCA
CTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGAGCACAGGTT
CGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAG
ATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCC
TTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAACATCGTGG
ACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCAATAATGGGA
GTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGCTTATGGA
TGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCTCAATGC
GGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTTGTGTTCTTCTGTGCTGCCT
GGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCCTTCTATGGCGTGTGGCC
GCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAAGCTT

SEQ ID NO 49 (HCC166)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCA
CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGC
GCAGGGGCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC
CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG
CTCAGCCCGGGTACCCTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG
GCTCCTGTCACCCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG
TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG
GGTACATTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG
CGTCCGGGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCT
TTCTCTATCTTCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAA
GTGCGCAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTG
TGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGA
GAACAACCTCTTCCCGCTGCTGGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCC
AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT
TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCTCGTCTCCAGCTG
TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC
CCGGCCACATAACGGGTACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTAC
AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTGCTGGACATGGTG
GCGGGGGCCCATTTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGA
GGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGT
GTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGG

Fig. 21L

TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT
GCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC
ACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAA
GTTGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG
CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT
GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT
TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC
ACGCGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTC
CCAAGACGTGTGGGGGCCCCCGTGAACATCGGGGGGGCCGGCAACAACACCTTGA
CCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC
TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC
CCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGC
ACAGGTTTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA
GGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC
CTGTTCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC
ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCATCA
AATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGC
TTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCC
TCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTTGTGTTCTTCTGT
GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATAACGCCTTCTATGGCG
TGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

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Fig. 22

OD measured at 450 nm
construct

Fraction	volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
START	23 ml	1/20	2.517	1.954	1.426	1.142
FLOW THROUGH	23 ml	1/20	0.087	0.085	0.176	0.120
1	0.4 ml	1/200	0.102	0.051	0.048	0.050
2			0.396	0.550	0.090	0.067
3			2.627	2.603	2.481	2.372
4			3	2.967	3	2.694
5			3	2.810	2.640	2.154
6			2.694	2.499	1.359	1.561
7			2.408	2.481	0.347	1.390
8			2.176	1.970	1.624	0.865
9			1.461	1.422	0.887	0.604
10			1.286	0.926	0.543	0.519
11			0.981	0.781	0.294	0.294
12			0.812	0.650	0.249	0.199
13			0.373	0.432	0.239	0.209
14			0.653	0.371	0.145	0.184
15			0.441	0.348	0.151	0.151
16			0.321	0.374	0.098	0.106
17			0.525	0.186	0.099	0.108
18			0.351	0.171	0.083	0.090
19			0.192	0.164	0.084	0.087

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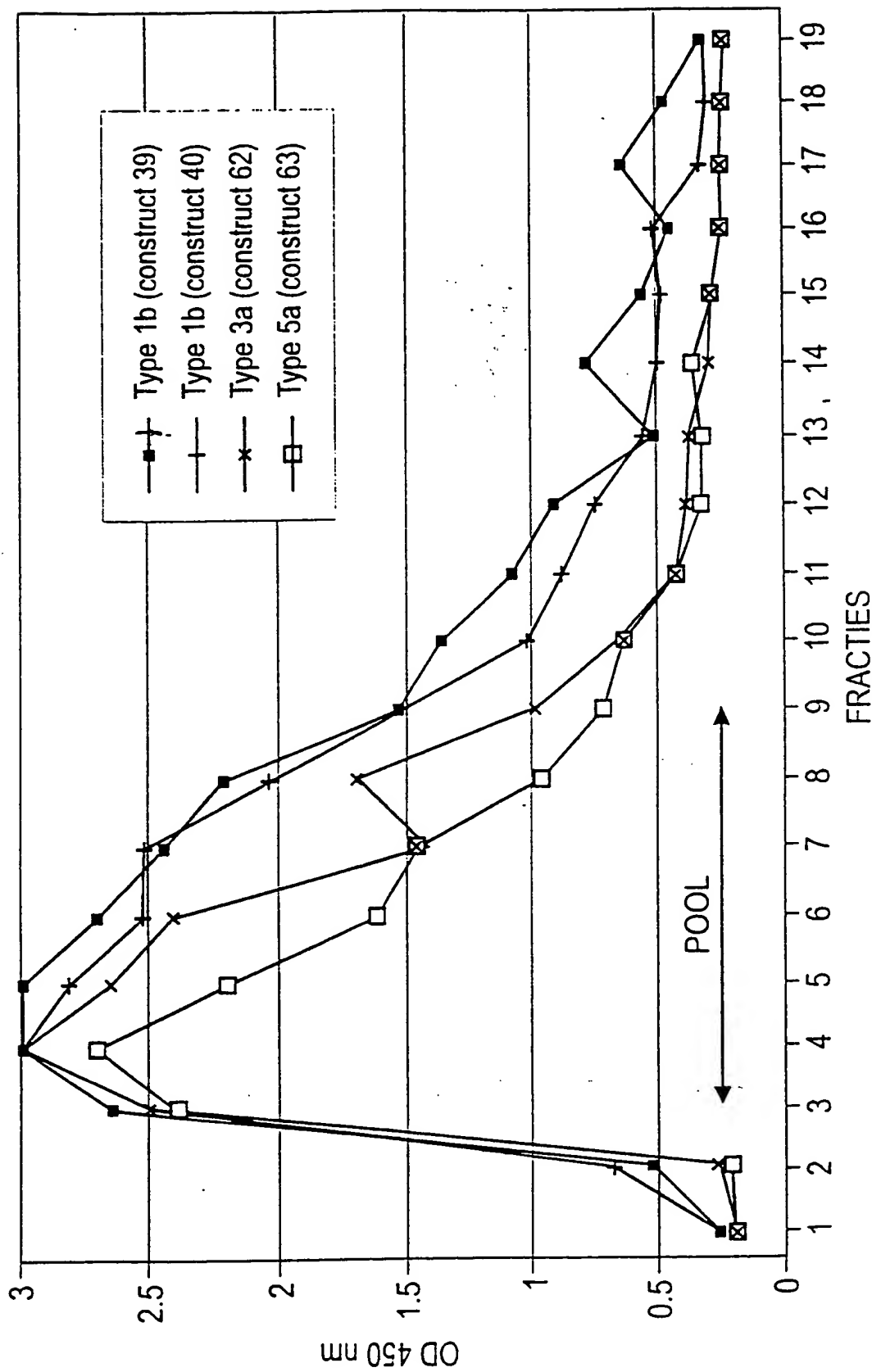


Fig. 23

100107 520E2650

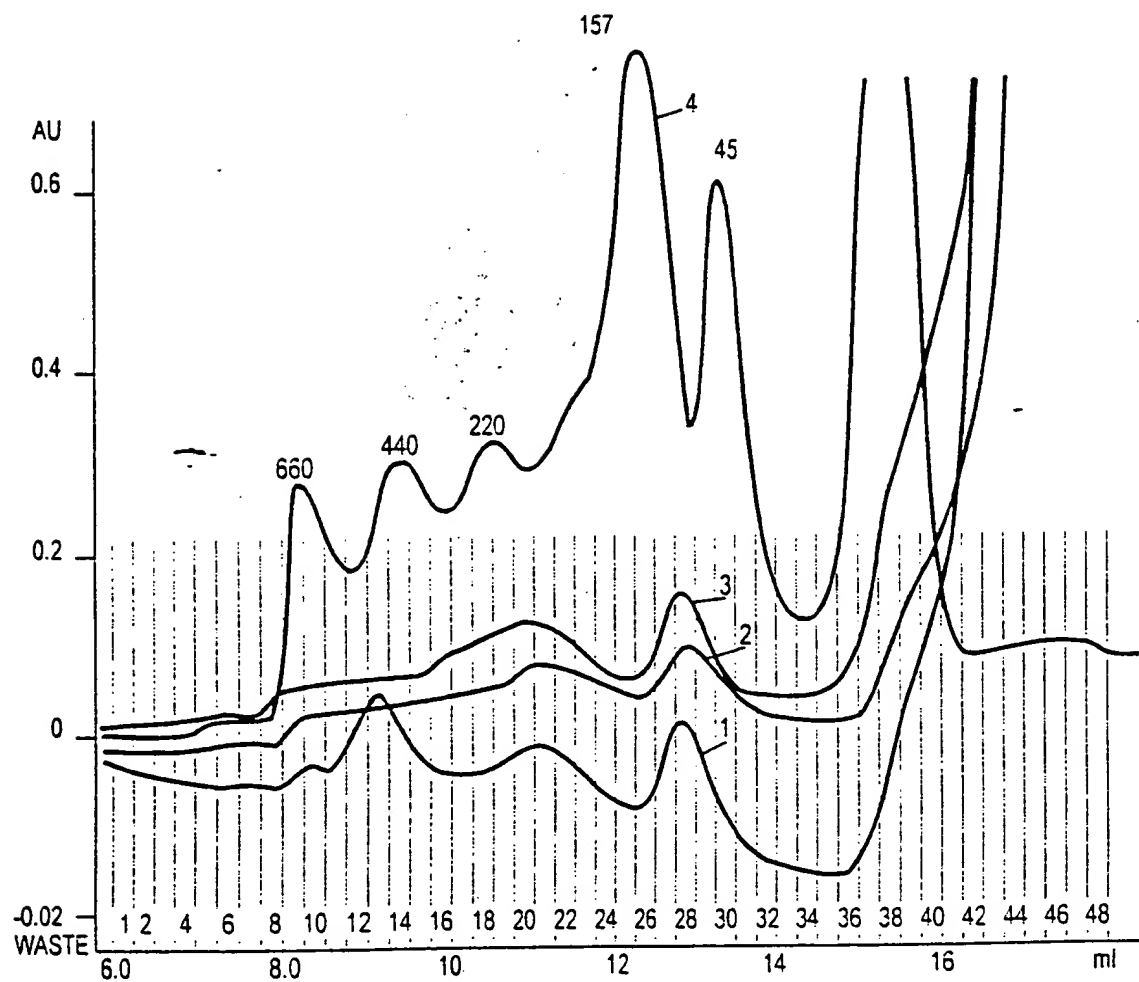


Fig. 25

09973025 101001

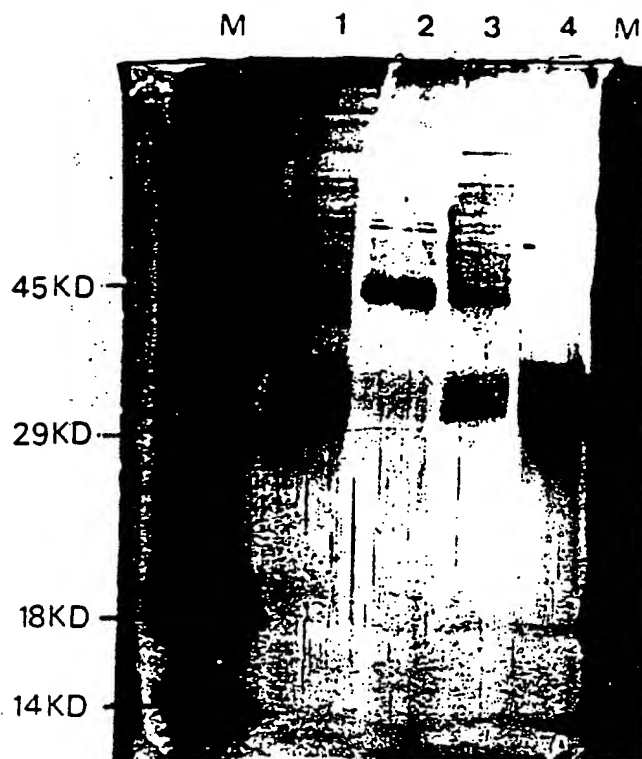


Fig. 26

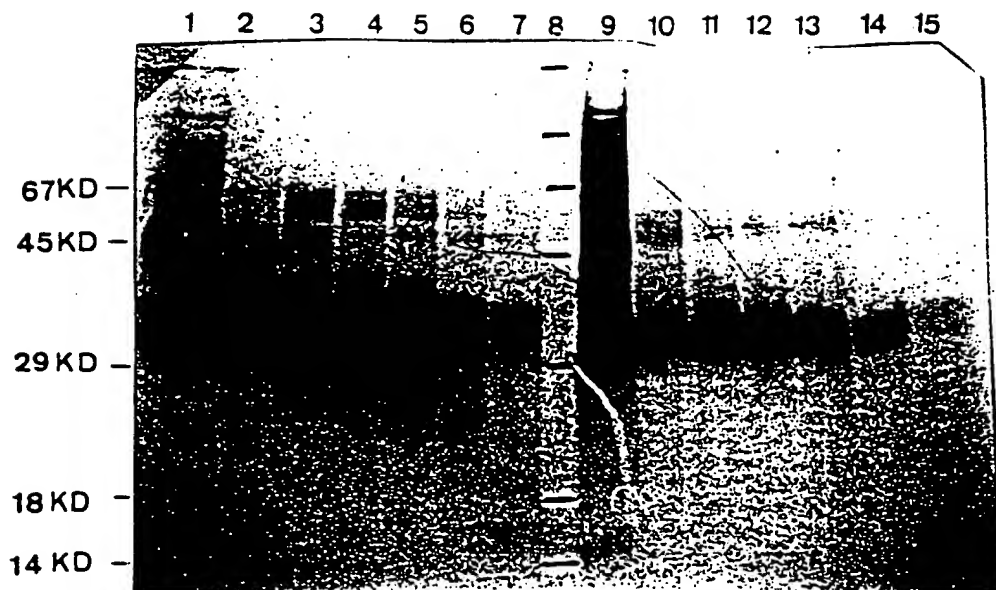


Fig. 27

09973025.101001

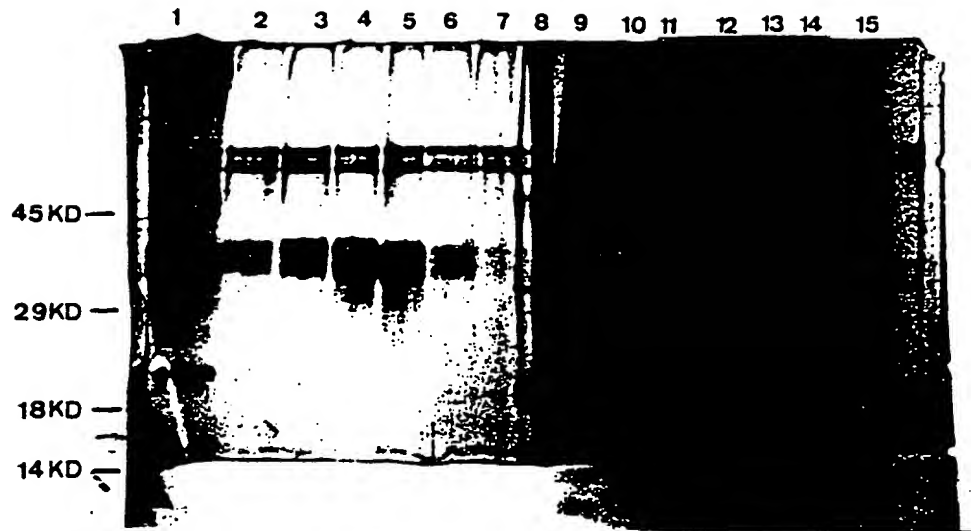


Fig.28

M 1 2 3 4 5 6

67 kD -

45 kD -

29 kD -

18 kD -

14 kD -

Fig.29

Lane 1: Crude Lysate
Lane 2: Flow through Lentil Chromatography
Lane 3: Wash with EMPIGEN Lentil Chromatography
Lane 4: Eluate Lentil Chromatography
Lane 5: Flow through during concentration lentil eluate
Lane 6: Pool of El after Size Exclusion Chromatography

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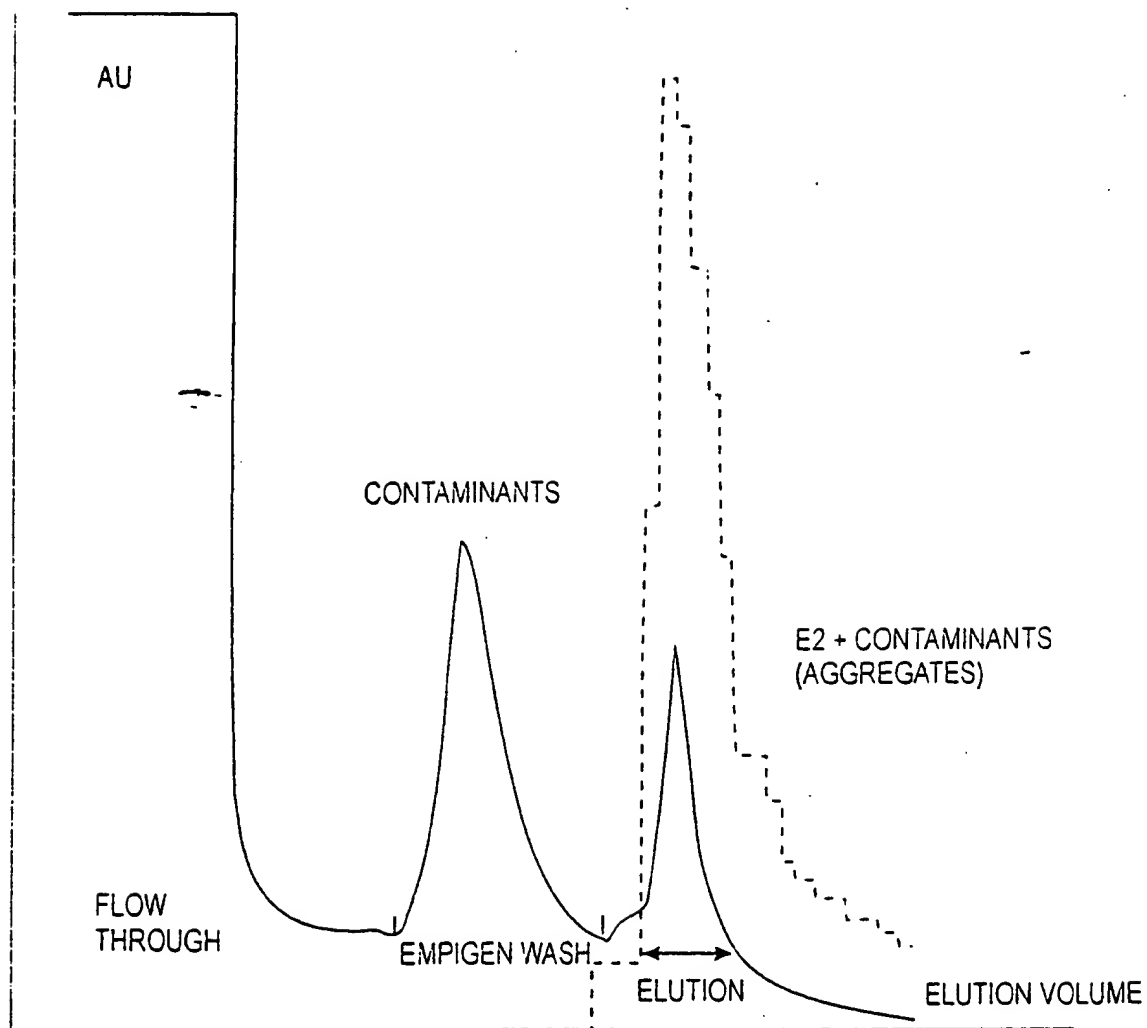


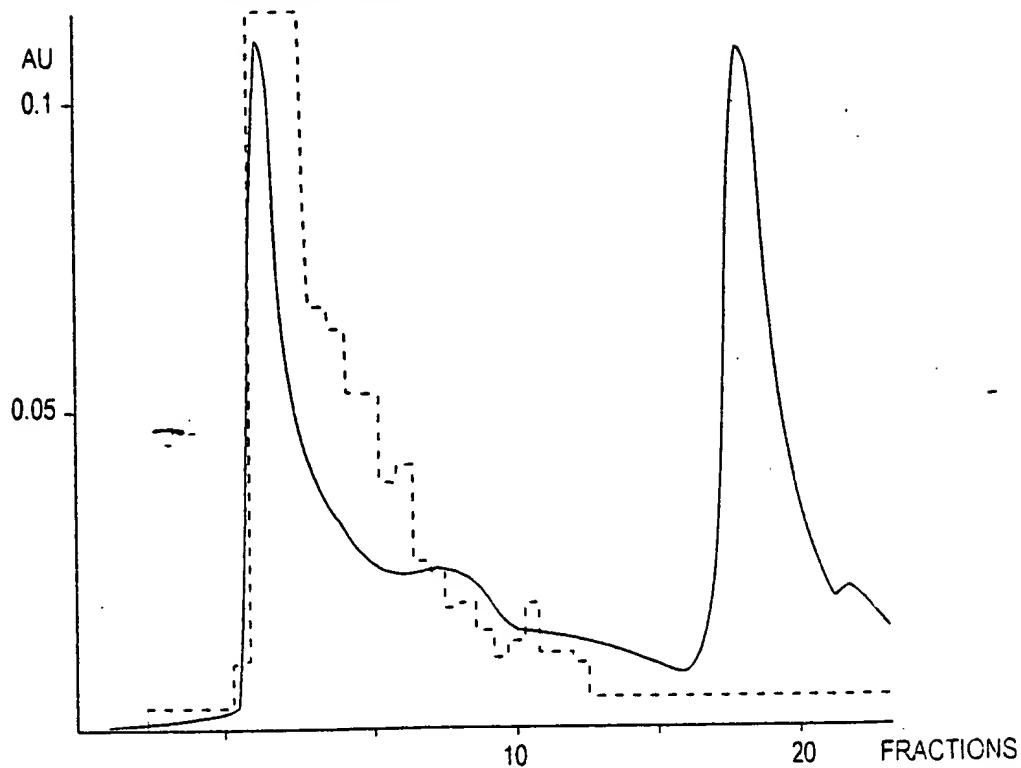
Fig. 30

09973025-101001

NON - REDUCED

Fig. 31A

E2 + CONTAMINANTS (AGGREGATES)



REDUCED

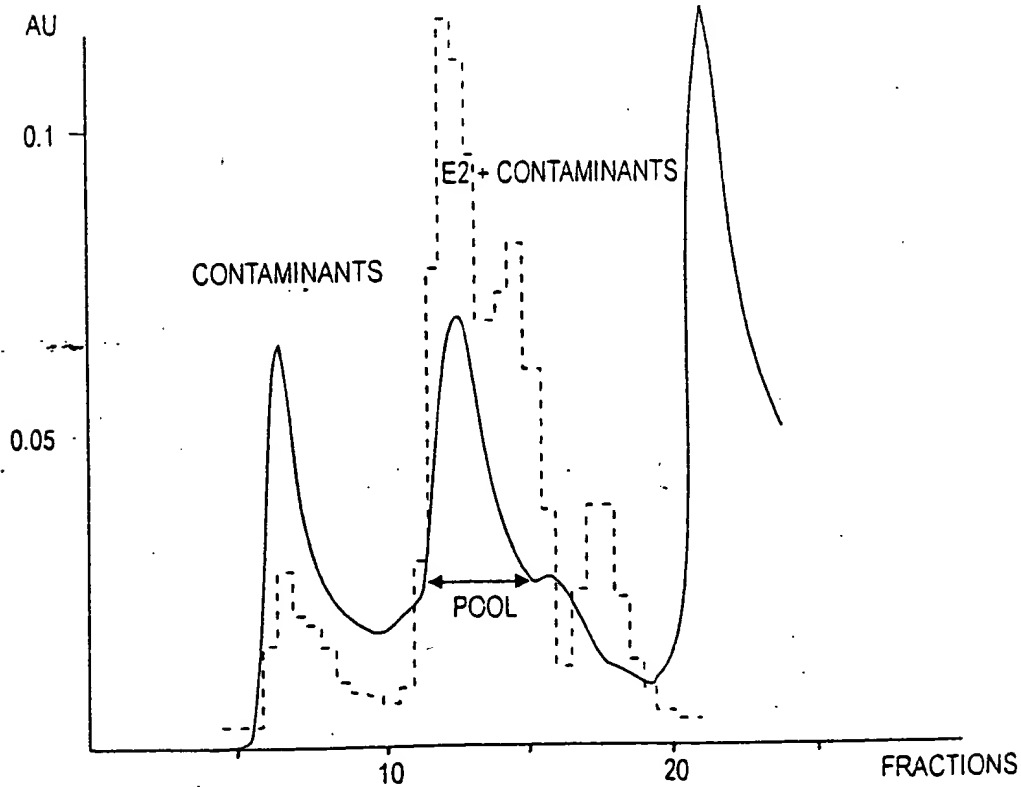


Fig. 31B

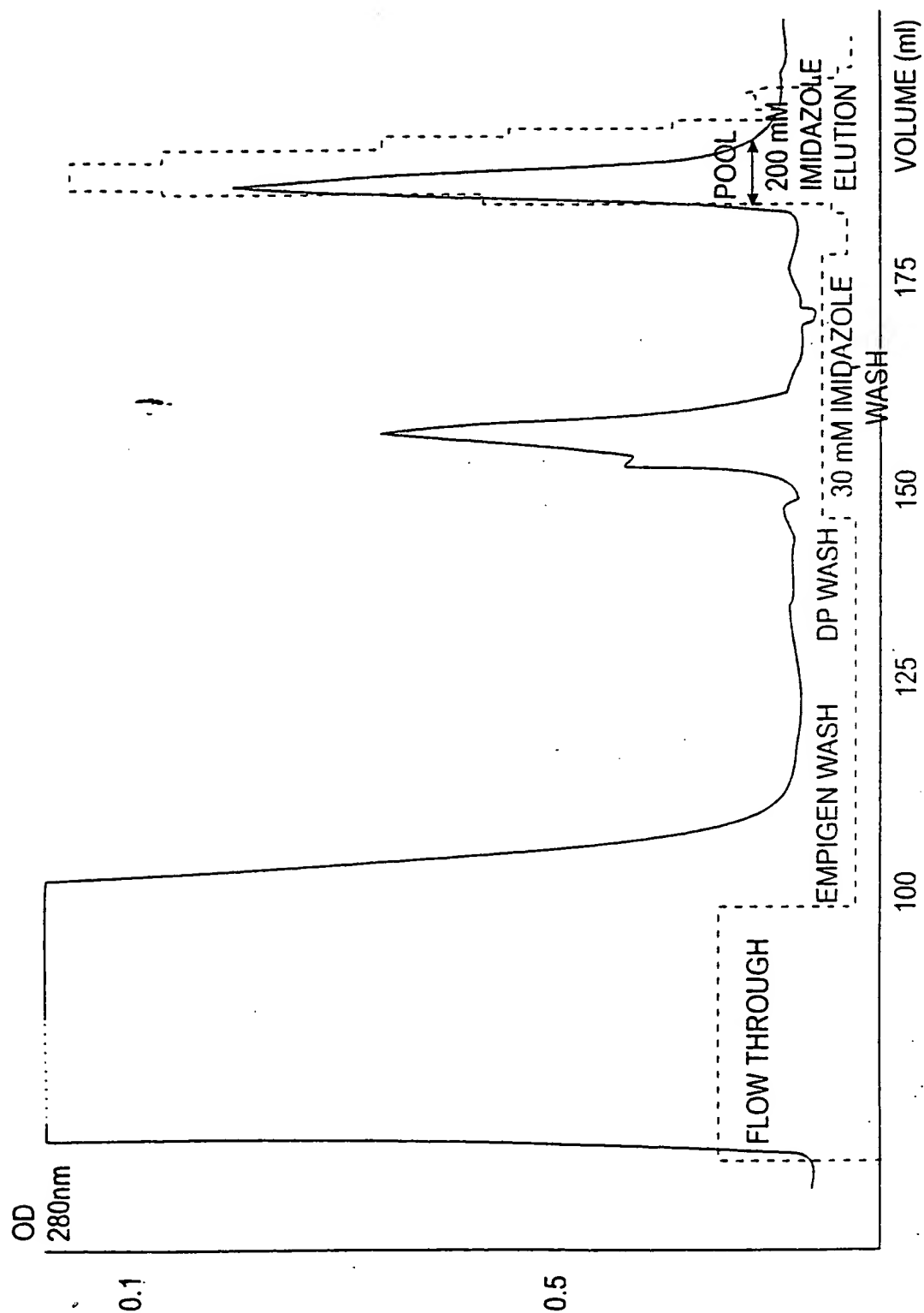
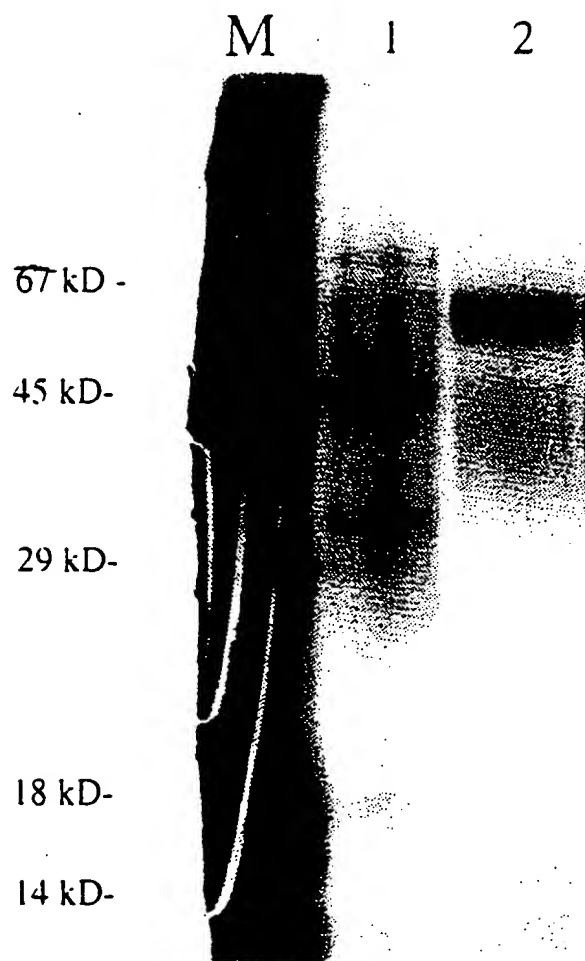


Fig. 32

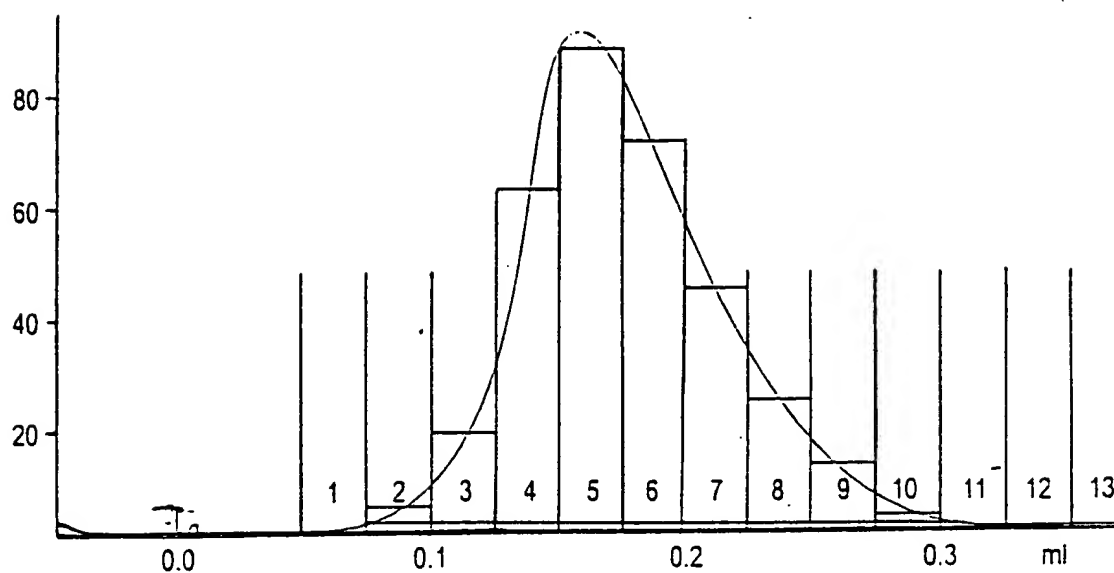
SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5 ug E2

Fig.33

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No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*AU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
 Total Area above baseline = 0.796522 ml*AU
 Total area in evaluated peaks = 0.796521 ml*AU
 Ratio peak area / total area = 0.999999
 Total peak duration = 2.613583 ml

Fig. 34

09973025-101004
FOUO - 520E2550

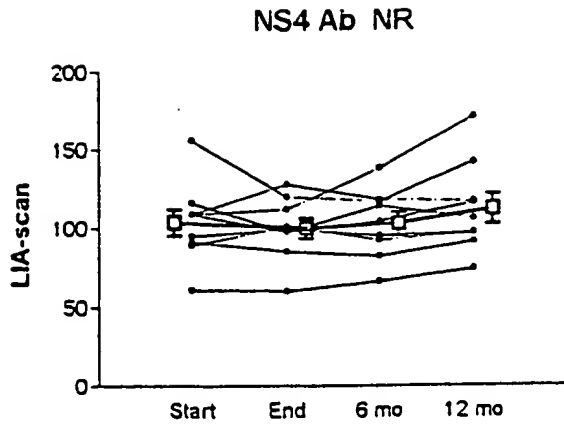


Fig. 35A-1

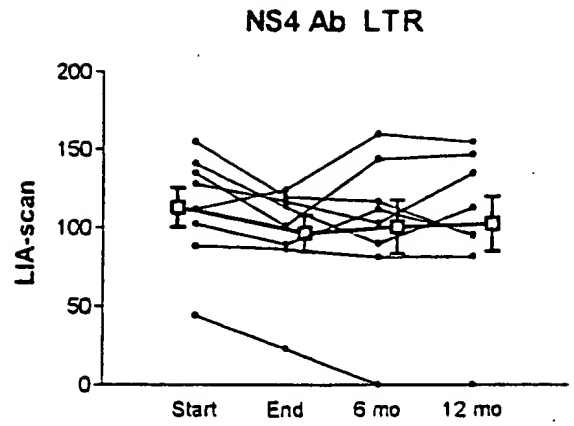


Fig. 35A-2

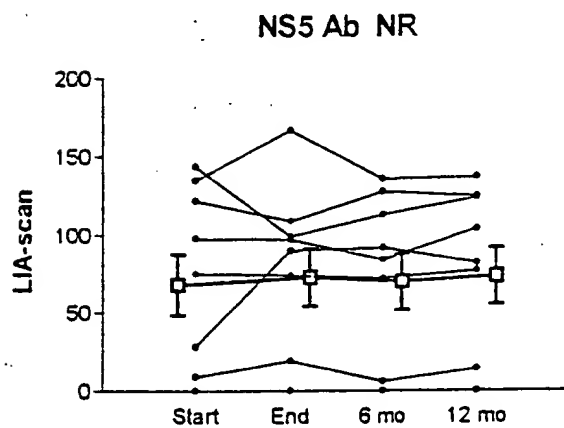


Fig. 35A-3

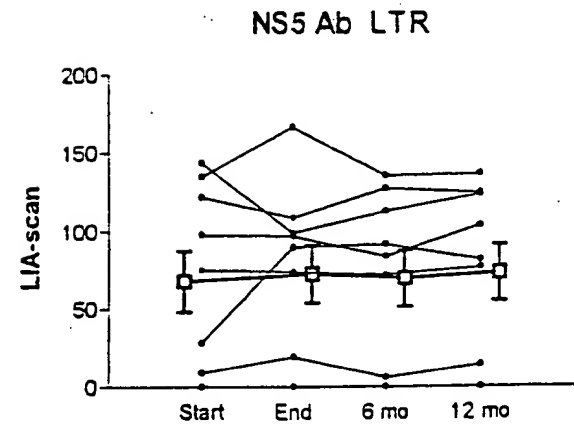


Fig. 35A-4

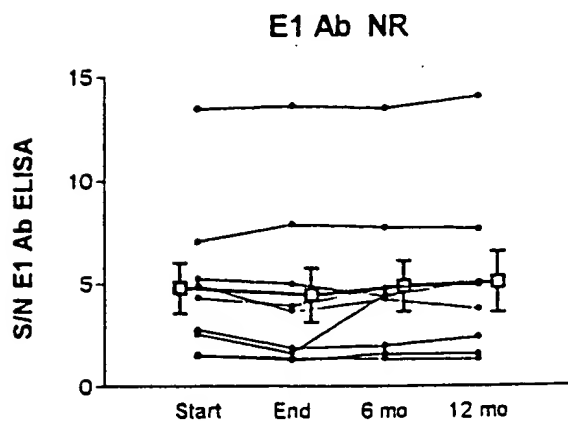


Fig. 35A-5

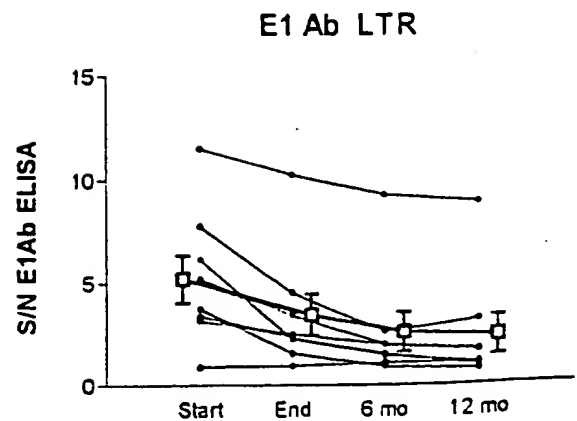


Fig. 35A-6

09973025 401001
T00T0T 520E2660

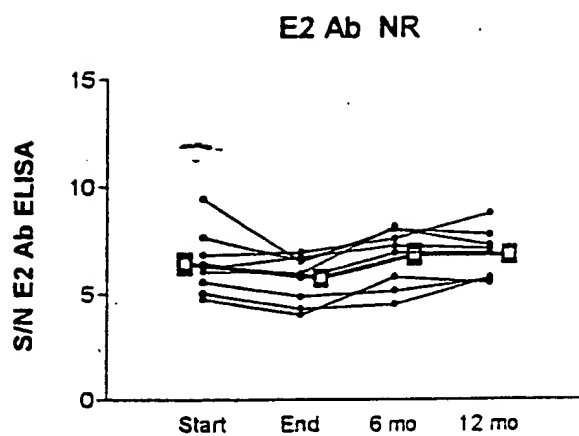


Fig. 35A-7

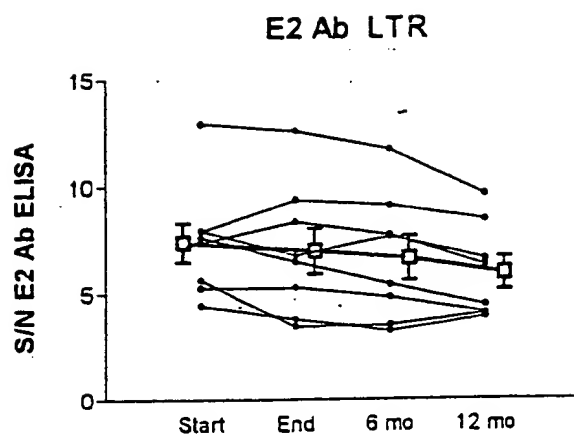


Fig. 35A-8

TOPOT-5205/660

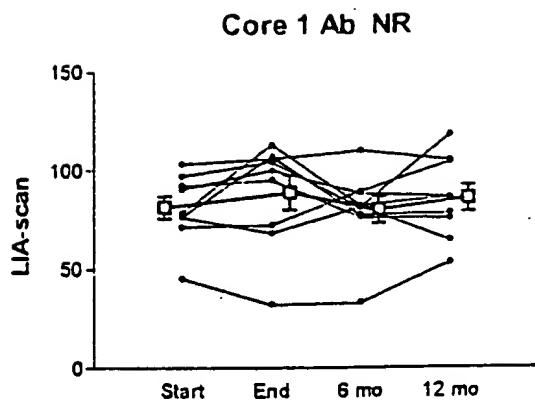


Fig. 35B-1

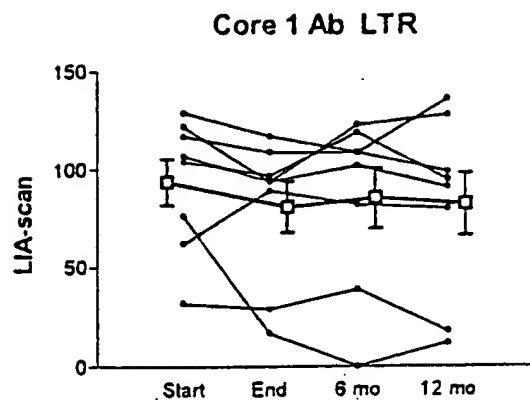


Fig. 35B-2

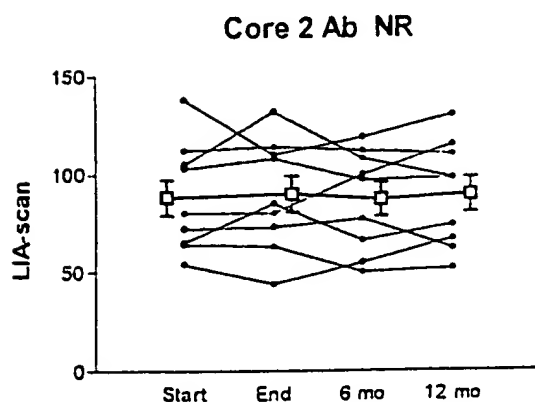


Fig. 35B-3

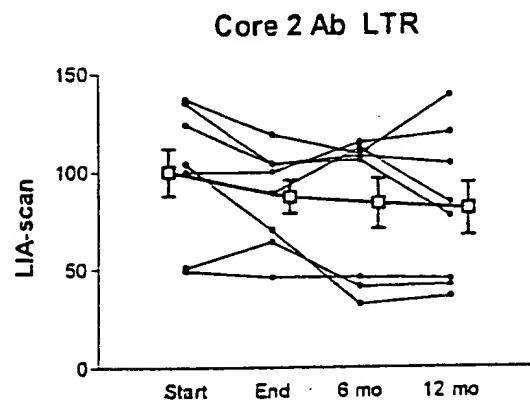


Fig. 35B-4

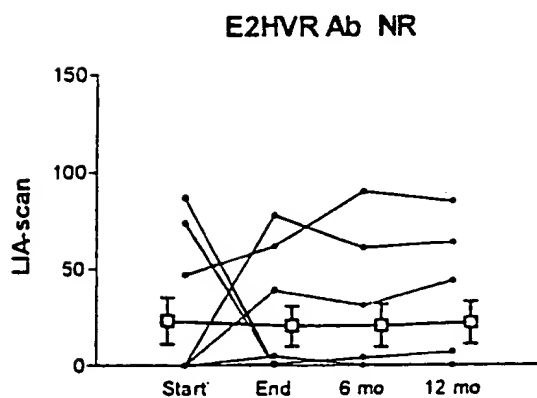


Fig. 35B-5

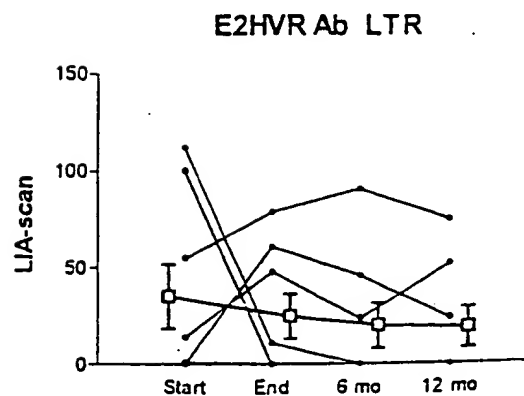


Fig. 35B-6

09973025-101001

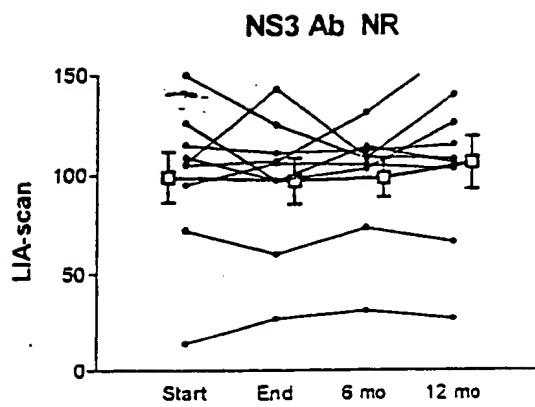


Fig. 35B-7

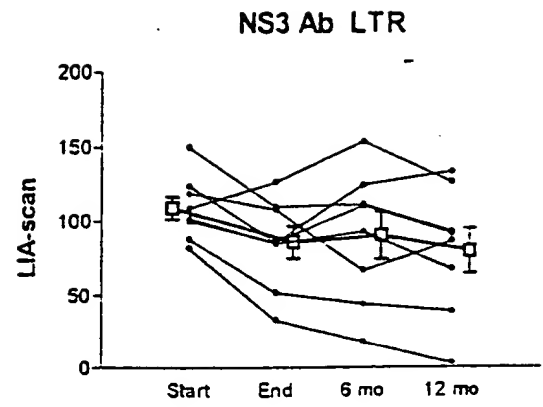


Fig. 35B-8

Fig. 36A

E1 Ab

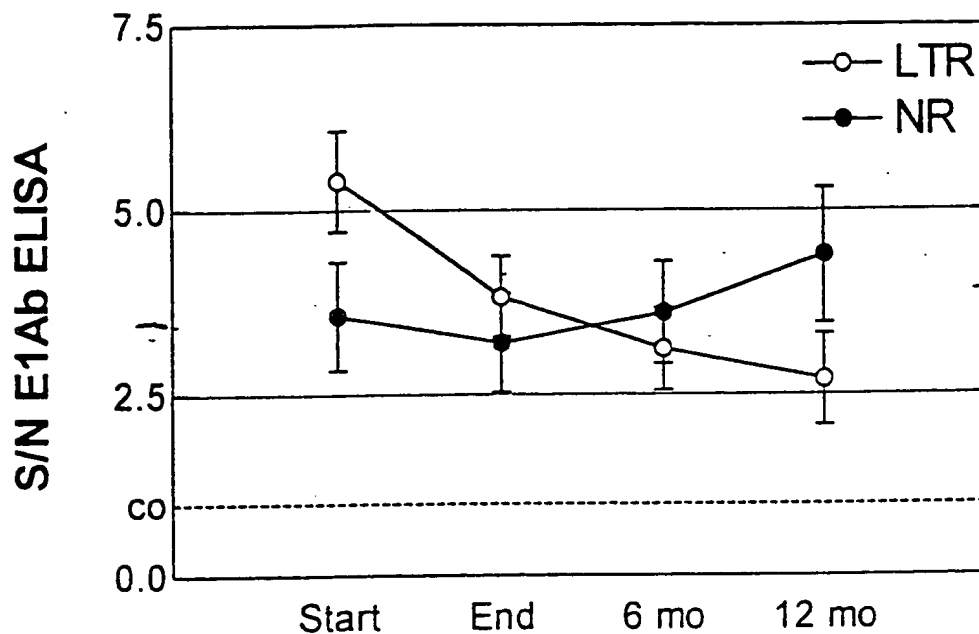


Fig. 36B

E2 Ab

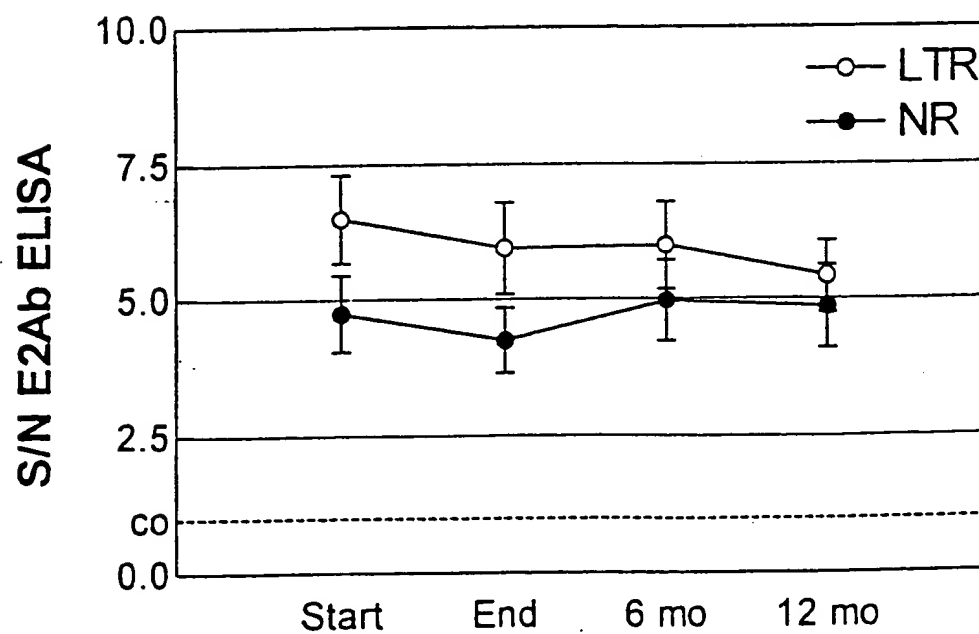


Fig. 37A
Non Responders

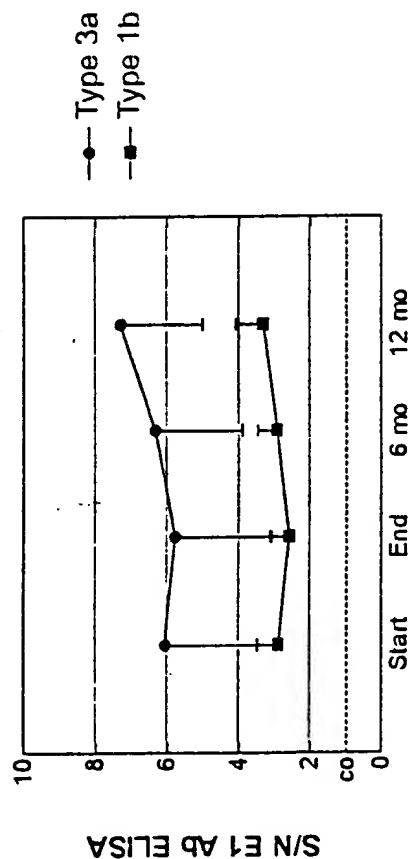


Fig. 37B
Long Term Responders

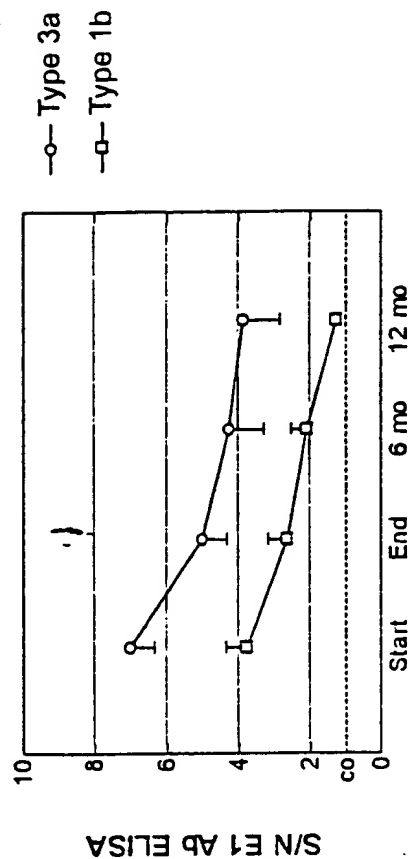


Fig. 37C
Type 1b

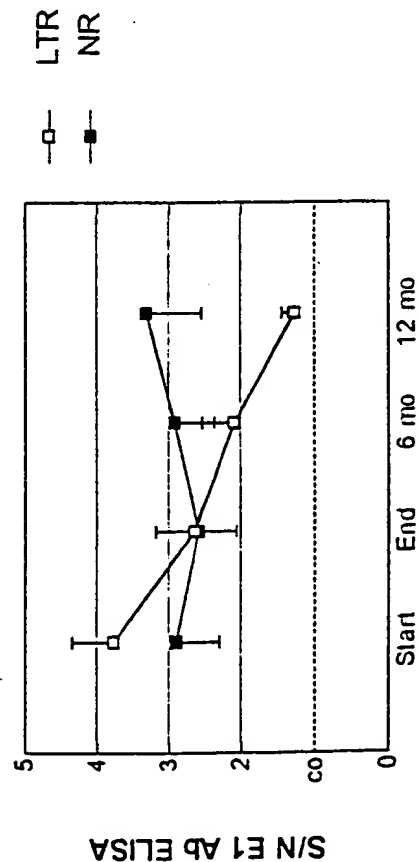
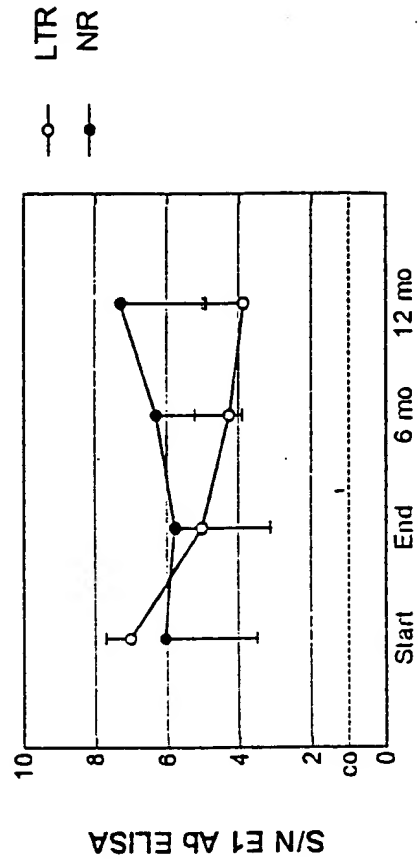


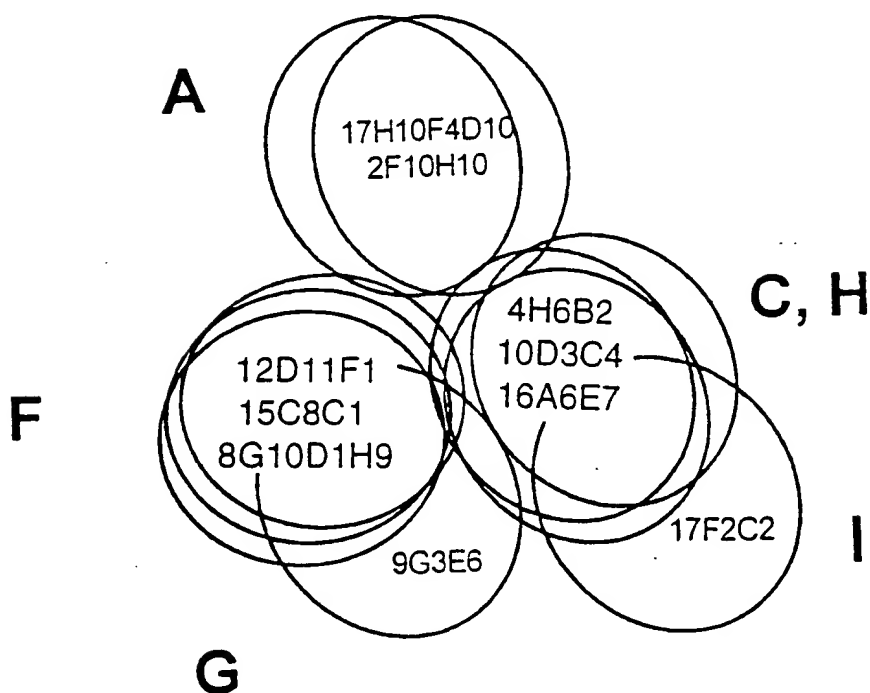
Fig. 37D
Type 3a



09973025.101001

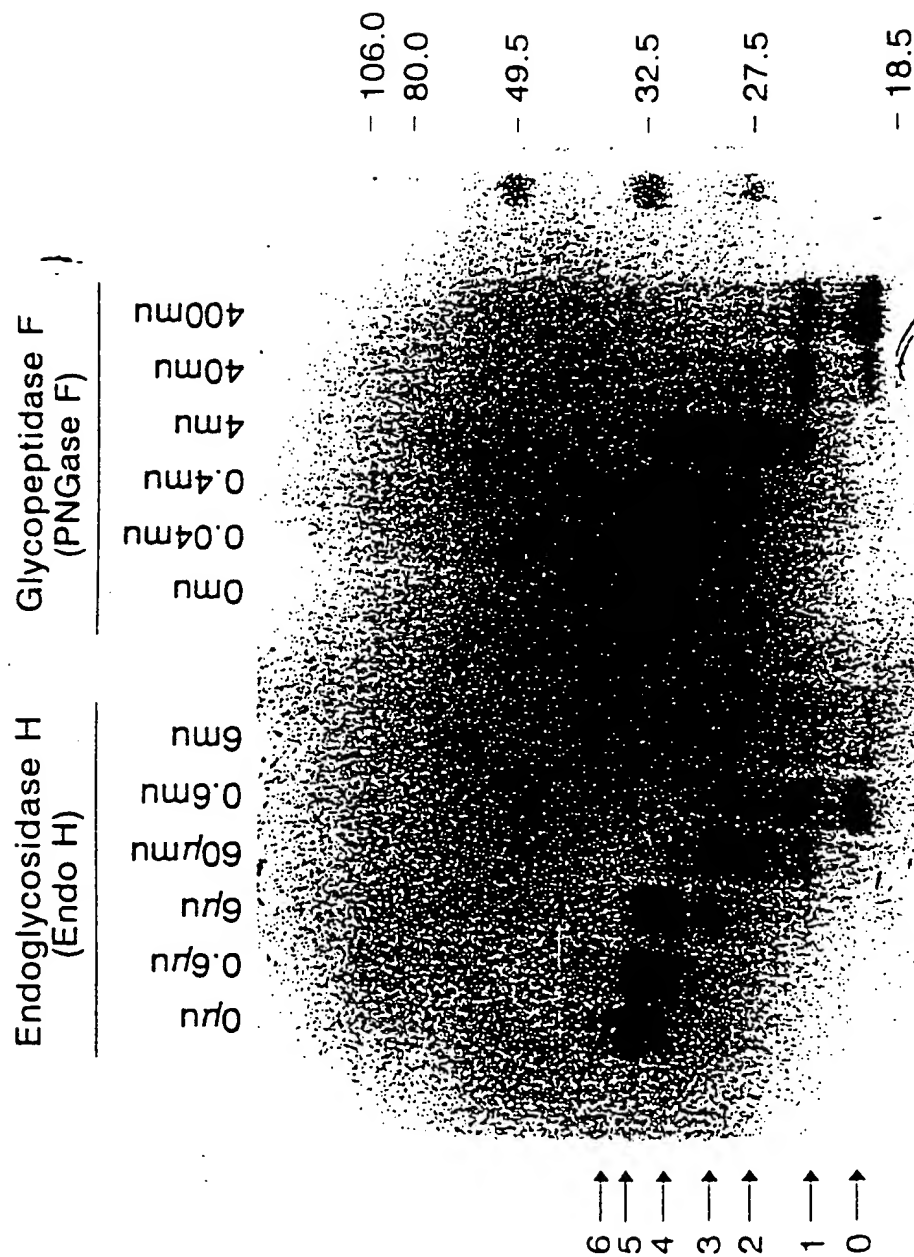
Fig. 38

Relative Map Positions of
anti-E2 monoclonal antibodies



PARTIAL DEGLYCOSYLATION OF HCV E1 ENVELOPE PROTEIN

Fig.39



PARTIAL TREATMENT OF HCV E2/E2s ENVELOPE PROTEINS BY PNGase F



Fig. 40

Fig. 41 *In Vitro* Mutagenesis of HCV E1 glycoprotein

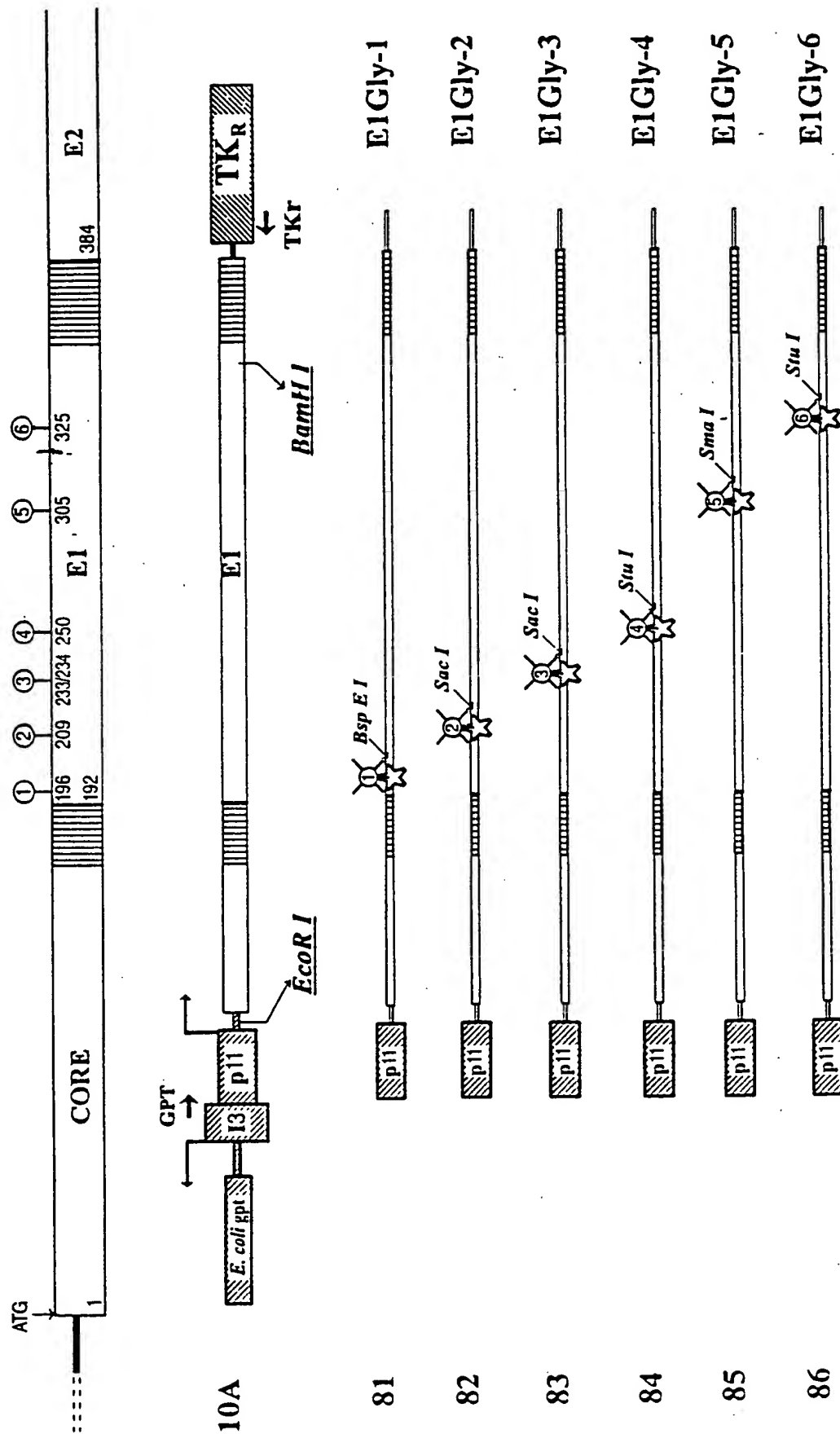
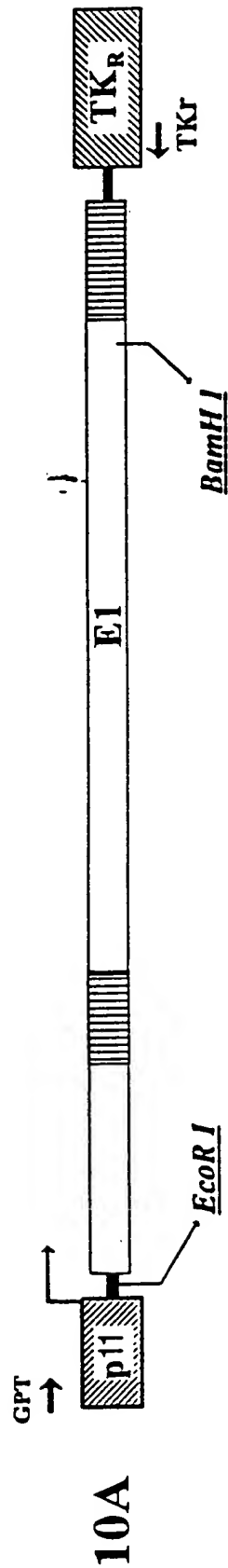
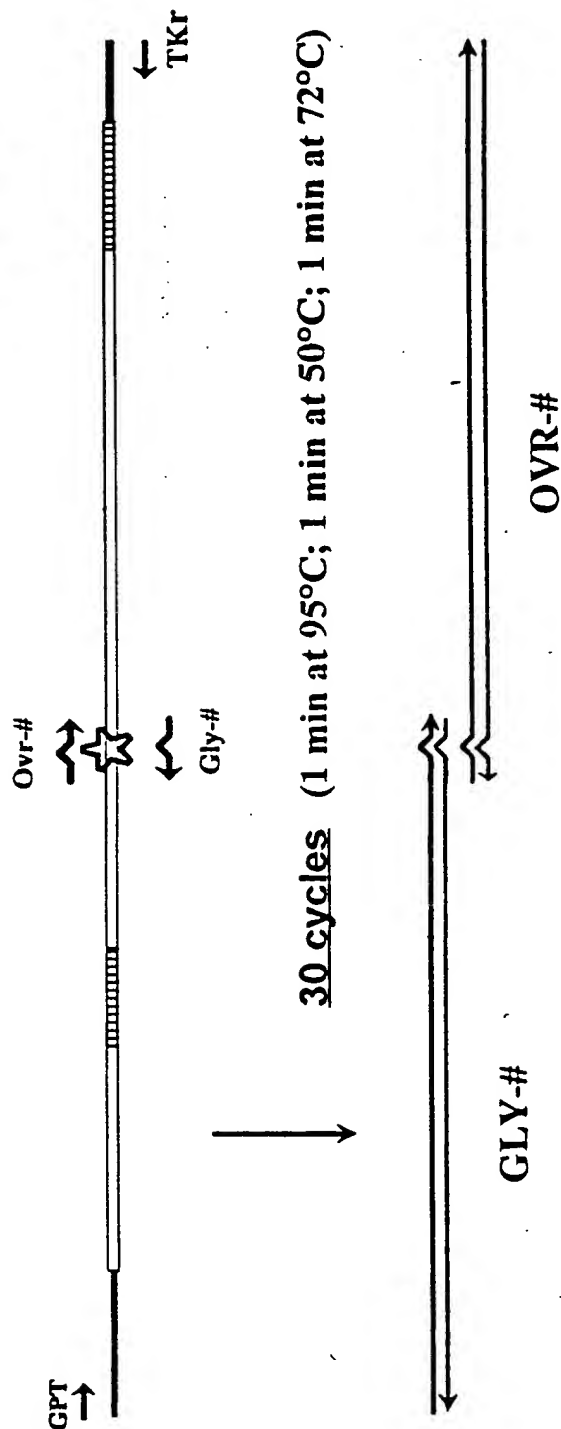


Fig. 42A *In Vitro* Mutagenesis of HCV E1 glycoprotein



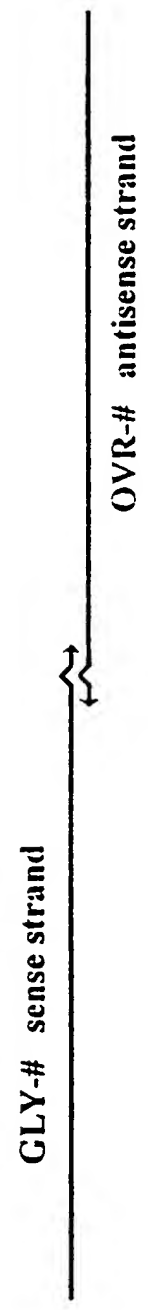
1. First step of PCR amplification (Gly-# and Ovr-# primers)



2. Overlap extension and nested PCR

Fig. 42B

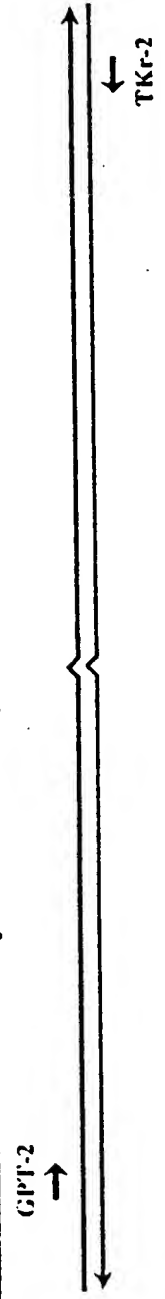
a. Overlap extension



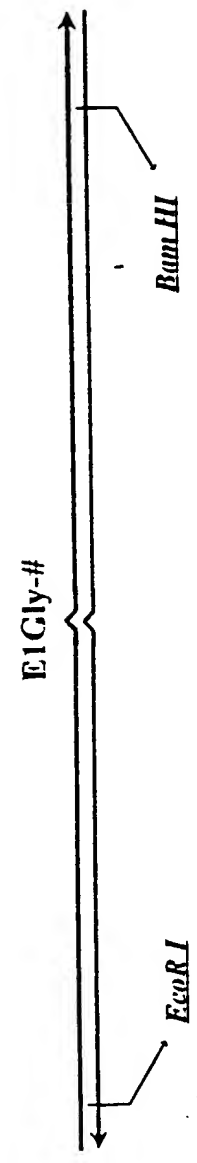
↓
2 cycles (1 min at 95°C; 1 min at 50°C; 1 min at 72°C)



b. Nested PCR amplification (GPT-2 and TKr-2 primers)



↓
25 cycles (1 min at 95°C; 1 min at 55°C; 1 min at 72°C)



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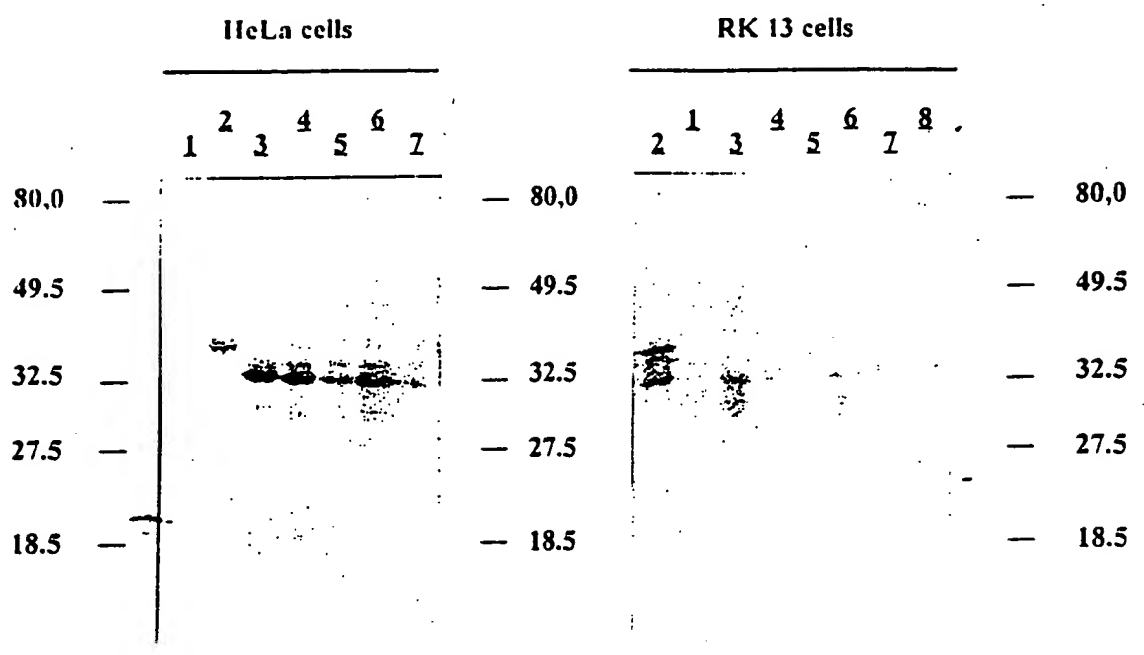


Fig. 44A



Fig. 44B

Fig.45

kDa 119 67 43 29 18

Fig.46

09973025-101001